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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, ex-  
pression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.



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## DESCRIPTION

Human Proteins Having Hydrophobic  
Domains and DNAs Encoding These Proteins

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## TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells  
10 expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic  
15 diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be  
20 utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be

25

## BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, and the like. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be expressed in the membrane. Therefore, when the amino acid sequence of a protein encoded by a cDNA when the



whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

5 OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells that are capable of  
10 expressing these DNAs and antibodies directed to these proteins. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

15

SUMMARY OF INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA  
20 bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of amino acid sequences 121 to 130. Moreover, the present invention provides a DNA  
25

encoding said protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150, an expression vector that is capable of expressing said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein and an antibody directed to said protein.

10 BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03171.

Fig. 2 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03424.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03444.

Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03478.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03499.

Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03500.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10691.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10703.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10711.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10712.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03010.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03576.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded

Fig. 14 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03612.

Fig. 15 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
5 by clone HP10407.

Fig. 16 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10713.

Fig. 17 illustrates the  
10 hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10714.

Fig. 18 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10716.

15 Fig. 19 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10717.

Fig. 20 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
20 by clone HP10718.

Fig. 21 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03745.

25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP03747.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10719.

5 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10720.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
10 by clone HP10721.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10725.

Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
15 by clone HP10727.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10728.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10730.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
25 by clone HP10742.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03800.

Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03831.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03879.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03880.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10704.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10715.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10724.

Fig. 38 illustrates the

Fig. 39 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10734.

Fig. 40 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
5 by clone HP10756.

Fig. 41 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03670.

Fig. 42 illustrates the  
10 hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03688.

Fig. 43 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03825

15 Fig. 44 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03877.

Fig. 45 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
20 by clone HP10765.

Fig. 46 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10766

25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP10770.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10772.

5 Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10773.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
10 by clone HP10776.

#### DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins  
15 from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequences of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the  
20 present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a  
25 carrying out in vitro translation using this RNA as a



template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present microorganism such as *Escherichia coli* etc., a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultivated, whereby the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein or the region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, 5 pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, Xenopus oocytes and the like. 10 Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the 15 liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in 20 the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, electrophoresis, 25 focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography, reverse phase chromatography and the like.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells and the addition of sugar chains to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a  
5 method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)<sup>+</sup> RNAs extracted from human cells as templates. The human cells may  
10 be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and  
15 Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can  
20 be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any section in the cDNA of the protein of the present invention. The cDNA of the protein of the present invention can be obtained by colony or plaque hybridization according to a method known  
25

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest  
5 are synthesized, which oligonucleotides are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71  
10 to 80, 101 to 110 and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Tables 1 and 2 summarizes the clone number (HP number), the cell from which the cDNA clone was obtained, the total number of bases of the cDNA, and the  
15 number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID NO.			HP number	Cell	Number of bases	Number of amino acid residues
1,	11,	21	HP03171	Thymus	2042	267
2,	12,	22	HP03424	Liver	1433	419
3,	13,	23	HP03444	Kidney	1917	415
4,	14,	24	HP03478	Umbilical cord blood	2258	380
5,	15,	25	HP03499	Kidney	1973	585
6,	16,	26	HP03500	kidney	1606	331
7,	17,	27	HP10691	Umbilical cord blood	2380	345
8,	18,	28	HP10703	Kidney	2017	89
9,	19,	29	HP10711	Kidney	1606	406
10,	20,	30	HP10712	Kidney	1695	192
31,	41,	51	HP03010	Kidney	1551	377
32,	42,	52	HP03576	Kidney	1713	81
33,	43,	53	HP03611	Kidney	1758	487
34,	44,	54	HP03612	Kidney	1550	375
35,	45,	55	HP10407	Stomach cancer	1485	350
36,	46,	56	HP10713	Kidney	2694	667
37,	47,	57	HP10714	Umbilical cord blood	3297	464
38,	48,	58	HP10716	Umbilical cord blood	2126	470
39,	49,	59	HP10717	Kidney	1781	243
40,	50,	60	HP10718	Umbilical cord blood	1788	270
61,	71,	81	HP03745	Kidney	1376	389
62,	72,	82	HP03747	Umbilical cord blood	2392	348
63,	73,	83	HP10719	Kidney	1416	261
64,	74,	84	HP10720	Kidney	1347	222
65,	75,	85	HP10721	Kidney	2284	183

Table 2

SEQ ID NO	HP number	Cell	Number of bases	Number of amino acid residues
66, 76, 86	HP10725	Kidney	1737	262
67, 77, 87	HP10727	Umbilical cord blood	1556	168
68, 78, 88	HP10728	Umbilical cord blood	1855	243
69, 79, 89	HP10730	Umbilical cord blood	2530	428
70, 80, 90	HP10742	Umbilical cord blood	1911	283
91, 101, 111	HP03800	Umbilical cord blood	1633	476
92, 102, 112	HP03831	Kidney	1095	226
93, 103, 113	HP03879	Kidney	1602	305
94, 104, 114	HP03880	Kidney	897	227
95, 105, 115	HP10704	Kidney	1866	441
96, 106, 116	HP10715	Umbilical cord blood	2198	265
97, 107, 117	HP10724	Umbilical cord blood	2180	208
98, 108, 118	HP10733	Umbilical cord blood	1527	400
99, 109, 119	HP10734	Umbilical cord blood	1905	192
100, 110, 120	HP10756	Kidney	998	260
121, 131, 141	HP03670	Umbilical cord blood	1622	337
122, 132, 142	HP03688	Umbilical cord blood	2475	236
123, 133, 143	HP03825	Kidney	1739	560
124, 134, 144	HP03877	Kidney	2005	406
125, 135, 145	HP10765	Umbilical cord blood	1558	453
126, 136, 146	HP10766	Kidney	1005	59
127, 137, 147	HP10770	Kidney	969	210
128, 138, 148	HP10772	Kidney	1241	165
129, 139, 149	HP10773	Kidney	1174	162
130, 140, 150	HP10776	Kidney	1012	221

5 libraries constructed from the human cell lines or human



tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

5 In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131  
10 to 150 shall come within the scope of the present invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as  
15 the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial  
20 base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA  
25 strand shall come within this scope. These DNA fragments can

be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide  
5 that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells  
10 into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom (JP-A 7-313187). Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention  
15 can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological  
20 activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration  
25 for example, in gene therapies or vectors suitable for

introduction of DNA).

#### Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques;

protein which binds or potentially binds to another protein

(such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell '75:791-803 (1993)) to identify polynucleotides  
5 encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-  
10 throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding  
15 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for  
20 example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.

25 agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: 10 Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or 15 supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be 20 administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium

Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro Assays for T-cell Proliferation, 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.

145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

5                    Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan  
10 eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

15                    Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology.  
20 J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988;

25                    Nordan, R. In Current Protocols in Immunology. J.E.e.a.

Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In  
5 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John  
10 Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include,  
15 without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines  
20 and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.



A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, lupus erythematosus, rheumatoid arthritis, autoimmune

pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and requires that the antigen has ceased. Operationally, tolerance can be demonstrated by

the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding antigen function such as T cells, and thus acts as an immunosuppressant.

Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be

Many autoimmune disorders are the result of inappropriate

activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Modulation of an antigen function (preferably a

immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and

enhancement of antigen function (preferably B lymphocyte

antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II with nucleic acid encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;



Chapter 7, Immunologic studies in Humans); Herrmann et al.,  
Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et  
al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.  
Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.  
5 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,  
1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-  
2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974,  
1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai  
et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.  
10 Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512,  
1988; Bertagnolli et al., Cellular Immunology 133:327-341,  
1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin  
responses and isotype switching (which will identify, among  
15 others, proteins that modulate T-cell dependent antibody  
responses and that affect Th1/Th2 profiles) include, without  
limitation, those described in: Maliszewski, J. Immunol.  
144:3028-3033, 1990; and Assays for B cell function: In  
vitro antibody production, Mond, J.J. and Brunswick, M. In  
20 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1  
pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will  
identify proteins that regulate predominantly  
25 described in: Current Protocols in Immunology, Ed by J. E.

Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W  
Strober, Pub. Greene Publishing Associates and Wiley-  
Interscience (Chapter 3, In Vitro assays for Mouse  
Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies  
5 in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;  
Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et  
al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will  
identify, among others, proteins expressed by dendritic  
10 cells that activate naive T-cells) include, without  
limitation, those described in: Guery et al., J. Immunol.  
134:536-544, 1995; Inaba et al., Journal of Experimental  
Medicine 173:549-559, 1991; Macatonia et al., Journal of  
Immunology 154:5071-5079, 1995; Porgador et al., Journal of  
15 Experimental Medicine 182:255-260, 1995; Nair et al.,  
Journal of Virology 67:4062-4069, 1993; Huang et al.,  
Science 264:961-965, 1994; Macatonia et al., Journal of  
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al.,  
Journal of Clinical Investigation 94:797-807, 1994; and  
20 Inaba et al., Journal of Experimental Medicine 172:631-640,  
1990.

Assays for lymphocyte survival/apoptosis (which  
lymphocyte homeostasis) include, without limitation, those  
25

described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby stimulating, for example, in treating various anemias stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Suitable assays for proliferation and

differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without  
5 limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

10 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I.  
15 Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I.  
20 Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay,  
25 York, NY. 1994; Long term bone marrow cultures in the

presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects and also is useful in cosmetic plastic surgery.

the treatment of periodontal disease, and in other tooth

repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful  
5 in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue  
15 is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to  
20 tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by  
25 repair of congenital, trauma induced, or other tendon or

ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries,

Parkinson's disease, Huntington's disease, amyotrophic



lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and  
5 cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to  
10 promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present  
15 invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for  
20 promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic

25 A protein of the present invention may also be

useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5           A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10           The activity of a protein of the invention may, among other means, be measured by the following methods:

          Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, 15 neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

          Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year 20 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

25           characterized by their ability to inhibit the release of

follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include,

782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et

al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have  
5 chemotactic or chemokinetic activity (e.g., act as a  
chemokine) for mammalian cells, including, for example,  
monocytes, fibroblasts, neutrophils, T-cells, mast cells,  
eosinophils, epithelial and/or endothelial cells.  
Chemotactic and chemokinetic proteins can be used to  
10 mobilize or attract a desired cell population to a desired  
site of action. Chemotactic or chemokinetic proteins provide  
particular advantages in treatment of wounds and other  
trauma to tissues, as well as in treatment of localized  
infections. For example, attraction of lymphocytes,  
15 monocytes or neutrophils to tumors or sites of infection may  
result in improved immune responses against the tumor or  
infecting agent.

A protein or peptide has chemotactic activity for  
a particular cell population if it can stimulate, directly  
20 or indirectly, the directed orientation or movement of such  
cell population. Preferably, the protein or peptide has the  
ability to directly stimulate directed movement of cells.  
Whether a particular protein has chemotactic activity for  
25 such protein or peptide in any known assay for cell

chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will  
5 identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for  
10 movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta  
15 Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### 20 Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a

25 as hemophilias) or to enhance coagulation and other

hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions  
5 resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity  
10 include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15           Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without  
20 limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation cell-cell  
ligands) and receptor/ligand pairs involved in antigen

presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein may inhibit tumor growth directly or indirectly



(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

10 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without  
15 limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);  
20 effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, carbohydrate, vitamins, minerals, proteins, lipids, and

nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the

Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

Human liver cDNA library (WO 98/21328) and human stomach cancer cDNA library (WO 98/21328), as well as the cDNA libraries constructed from human kidney mRNA (Clontech), human thymus mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, J. F., J. Biol. Chem. 257: 3225-3232 (1982)]. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

5           The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T<sub>N</sub>T rabbit reticulocyte lysate kit (Promega). In this case, [<sup>35</sup>S]methionine was added to label the expression product with a radioisotope. Each of the reactions was  
10           carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T<sub>N</sub>T rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached  
15           to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [<sup>35</sup>S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsomal fraction  
20           (Promega) to the reaction system. To 3 µl of the reaction solution was added 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol)  
25           and then subjected to SDS polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

*Escherichia coli* cells harboring the expression vector for the protein of the present invention were  
5 cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture medium containing 100 µg/ml of ampicillin, the helper phage M13KO7 (50 µl) was added thereto, and the cells were then  
cultured at 37°C overnight. Single-stranded phage particles  
10 were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO<sub>2</sub> in the  
15 Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum.  $1 \times 10^5$  COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 37°C for 22 hours in the presence of 5% CO<sub>2</sub>. After the medium was removed, the cell surface was washed with a phosphate  
20 buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl of the single-stranded phage suspension, 0.6 ml of the DMEM  
25 presence of 5% CO<sub>2</sub>. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO<sub>2</sub>. After the medium was exchanged for a medium containing

5    [35S]cysteine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

#### (4) Preparation of Antibodies

10            A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na<sub>2</sub>HPO<sub>4</sub>, 2 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.2) to a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus-prepared plasmid solution in

15    PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,

20    and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN<sub>3</sub> was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The preparation of an antibody was confirmed by

25    vector had been introduced or by Western blotting using a

cell lysate or a secreted product.

(5) Clone Examples

<HP03171> (SEQ ID NOS: 1, 11 and 21)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP03171 obtained from cDNA library of  
human thymus revealed the structure consisting of a 90-bp  
5'-untranslated region, a 804-bp ORF, and a 1148-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
267 amino acid residues and there existed one putative  
10 transmembrane domain. Figure 1 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 34 kDa that was somewhat larger than the molecular weight  
15 of 30,234 predicted from the ORF. In this case, the  
addition of a microsome led to the formation of a product of  
38 kDa. In addition, there exists in the amino acid sequence  
of this protein one site at which N-glycosylation may occur  
(Asn-Thr-Thr at position 169).

20 The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to chicken putative transmembrane  
protein. The amino acid sequence of the present protein is  
shown in SEQ ID NOS: 1, 11 and 21. The amino acid sequence  
of the present invention (HP) and chicken putative

25 of the present invention (HP) and chicken putative

transmembrane protein E3-16 (GG). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.0% in the entire region.

Table 3

---

10 HP MVKISFQPAVAGIKGDKADKASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY  
 \*\*\*.\*\*.\*.\* . \*.\*..... . \*. \*.\*.. .. \*.  
 GG MVKVSFNSALAH--KEAANKEEENSQVL-ILPPDAKEPEDVVVPAGHKRAWCWCM---CF

HP LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL-----SSQVRTQM--  
 15 \*.. .\* \*.....\*.\*.\*\* ..\* . .\* \*\*. \* \*\*.\* ..\*.....  
 GG ---GLAFMLAGVILGGAYLYKYFAFQQ--GGVYF-CGIKYIEDGLSLPESGAQLKSARYH

HP ELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTI  
 ..\*....\* .\*. \* \*.\*\*\*\*.\*...\*\*\*\*.\* \*\*.\* \*\*.\* \*.\*\*\*\*\*\* \*\*.\*.  
 20 GG TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV

HP VLPPRNFWEELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRR  
 \* \*\* \*\* \*\* \*



HP RATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

..... \*.\*\*.\* \*\*. \*\*\*\*\* \*.\*\*\*\*\*

GG KEAMKGIQKREAVNCRKIRHFENRFAMETLICEQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL036384) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03424> (SEQ ID NOS: 2, 12 and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03424 obtained from cDNA library of human liver revealed the structure consisting of a 4-bp 5'-untranslated region, a 1260-bp ORF, and a 169-bp 3'-untranslated region. The ORF encodes a protein consisting of 419 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the method of Kyte and Doolittle (1982), of the present protein. In vitro

of 50 kDa that was somewhat larger than the molecular weight

of 46,375 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein six sites at which N-glycosylation may occur (Asn-Ala-Ser at position 29, Asn-Val-Thr at position 40, Asn-Cys-Thr at position 112, Asn-Lys-Ser at position 135, Asn-Ile-Ser at position 172 and Asn-Phe-Ser at position 189). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from aspartic acid at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH protein (Accession No. Q06003). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster* GOLIATH protein (DM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the intermediate region of 212 amino acids.

Table 4

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	HP	MSCAGRAGPARLAALALLTCSLWPARADNASQEYYTALINVTVQEPGRGAPLTFRIDRGR
5	HP	YGLDSPKAEVRGQVLAPLPLHGVADHLGCDPQTRFFVPPNIKQWIALLRGNCTFKEKIS
	HP	RAAFHNAVAVVIYNNKSKEEPVTMTHPGTGDI IAVMITELRGKDILSYLEKNISVQMTIA
		. * ** . . . * . * . * . * . * . . *
	DM	MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGYNTISII
10	HP	VGTR--MPPKNFSRGS�VFSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRRLGDA
		* * . . . . * . * . * * * * * * . * . * * * * * . * . * . * . * . .
	DM	EGRRGVRTISSLNRTSVLFVSISFIVDDIL---CWLIFYIQRFRYMQAKDQQSRNLCSVT
15	HP	KKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDPWLSEH
		**** * . * . * * . * * . * * * * * * . * . * * * * * * * * . * . * * * * *
	DM	KKAIMKIPTKTGKFSD-EKDLSDCCAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIEH
	HP	CTCPMCKLNILKALGIVPNLPCTDNVAFDMERLTRTQAVNRRSALGDLAGDNSLGLEPLR
20		***** . ** * * . . . . . . . . . . . . . . . * . ** .
	DM	RTCPMCKLDVLKFYGYVVGDIYQTPS--PQHTAPIASIEEVPVIVVAVPHGPQPLQPLQ
	HP	TSCIGDI DDCGELTDRTCINIAVTRKXVLIAGDILLGALTLCVLLDRTATLMAVHVV
25	DM	ASNSSSFAPSHYFQSSRSFSSSVQQQLAPLTYQPHPQQAASERGRRNSAPATMPHAITAS

HP F

DM HQVTDV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA082118) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03444> (SEQ ID NOS: 3, 13 and 23)

15

Determination of the whole base sequence of the cDNA insert of clone HP03444 obtained from cDNA library of human kidney revealed the structure consisting of a 209-bp 5'-untranslated region, a 1248-bp ORF, and a 460-bp 3'-untranslated region. The ORF encodes a protein consisting of 415 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

20

25

of 43 kDa that was somewhat smaller than the molecular

weight of 45,691 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 42 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 24.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human type I procollagen C-proteinase enhancer protein (Accession No. BAA23281). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human type I procollagen C-proteinase enhancer protein (CP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.6% in the entire region.

Table 5

---

HP	M	R	G	A	N	A	W	A	P	L	C	L	L	A	A	T	Q	L	S	R	Q	Q	S	P	E	R	P	V	F	T	C	G	G	I	L	T	G	E	S	G	F	I	G	S	E	G	F	P	G	V	Y	P
----	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

HP PNSKCTWKITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNGH-ANGQRIGRFCGTFRPG

\*\*. \*. \*. \*\*\*\*\*. \*. \*. \*\* . \*\*\* . \*\*\*\* .. \*. \* .. \*\*\*. \*\*\*\*\*.

CP PNKECIWTITVPEGQTVSLSFRVFDLELHPACRYDALEVFAAGSGTSGQRLGRFCGTFRPA

5 HP ALVSSGNKMMVQMISDANTAGNGFMAMFSAEPNERGDQYCGLLDRPSGSFKTPNWPDR

. \*\*. \*\*. . . \*. \*. \*. \*. \*. \*. \*. \*. . \*. . . . . \*. \*\*\* \*. . . \*. . . \*\*\*\*\*.

CP PLVAPGNQVTLRMTTDEGTGGRGFLLWYSGRATSGTEHQFCGGRLEKAQGTLTTPNWPES

HP DYPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGD

10 \*\*\*. \*. \* \*\*\*. \*\* . \*. \*. \*. \*\*\*\*\*. \*. \*. \*\*\*\*\* \*. \*\*\*\*. . \*. \*\*. \*\*. \*\*\*

CP DYPPGISCSWHIIAPPDQVIALTFEKFDLEPDITYCRYDSVSVFNGAVSDDSRRLGKFCGD

HP SPPAPIVSEARNELLIQFLSDLSTADGFIGHYIFRPKKLPTTTE-----

. \*. \* \* \* \*\*\*\*. \*\*. \*\*\*\*. \*\*\*\*\* . \* \*. . . . .

15 CP AVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKGQGPGRGTETPKVKLPP

HP QPVTTTTFPVTTGLKTTVALCQQKCRRTGTLEGNYCSSDFVLAGTVITTITRDG-SLHATV

.. . . . . . . . . . . \*. . . \*\*\*\*\*. \*. \*. \*. \*. \*. \*. \*. . . . \*. \*. \*\*

CP KSQPPEKTEESPSAPDAPTCPKQCRRTGTLSNFCASSLVVTATVKSMVREPGGLAVTV

20

HP SIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRGLNYIIMGQVGEDGRGKIM-PNSF

\*. \*. \*\*. \*. \*. . . . . \* .. \* \*\*\*\*\* .. \*. \*. \*. \*\*\*\*\* \*. \*. \*\* .. \*. \*\*

CP SLICAYKTCGLDPSRPTCASLKEYVDCVCKOCDNKKKQCVLLGCGV LKNDGCVLLGCGV

25

HP IMMFKTKNQKLLDALKNKQC

... ..\*..\*....\*

CP VVLRPNQDQILTNLSKRKCPSQPVRAAASQD

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5           The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. D78874) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
10 encode the same protein as the protein of the present  
invention.

<HP03478> (SEQ ID NOS: 4, 14 and 24)

Determination of the whole base sequence of the  
cDNA insert of clone HP03478 obtained from cDNA library of  
15 human umbilical cord blood revealed the structure consisting  
of a 224-bp 5'-untranslated region, a 1143-bp ORF, and a  
891-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 380 amino acid residues and there existed five  
putative transmembrane domains. Figure 4 depicts the  
20 hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product

25       acid sequence of the present protein revealed that the

protein was similar to Halocynthia roretzi HrPET-1 protein (Accession No. BAA81907). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Halocynthia roretzi HrPET-1 protein (HR). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.8% in the entire region.

Table 6

---

HP	MLQTLYDYFWWERLWLPVNLTWADLEDGRVYAKASDLYITLPLALLFLIVRYFFEL
15	. * . * * . * * * . * . * * * . * * . * * . * * . * . * . *
HR	MDLLMDLYHWFNEKFWLPQNLTWEDLKRTEEKQFGETRDLWLTPLCITVLCIRFSVEK
HP	YVATPLAALLNIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWF
	. * * * . * * . * . * . * . * . * . * . * . * . * . * . *
20	HR GIARPLGKWLNLSERLHTPPRENIVLEKVYKTITRKNYSQVEDLCKQTGWRKHEINVWF
HP	RRRRNQDRPSLLKKFREASWRFTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPS
	* *



HP Q-YWYYMIELSFYWSLLFSIASDVKRKDFKEQIIHHVATIILISFSWFANYIRAGTLIMA

. \*.\*\*,\*\*\*.\*\* . . . \*\*\*\*\* \* .\*\*\*.\*\*\*. . \*. \*\*..\*..\*..

HR KIIYYYLIELAFYSATTLTQFFDVKRKDFWEMFIHHIVTIILLCGSYTLNYTKMGAFILV

5 HP LHDSSDYLLES AKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYPLELYP

.\*\*\*.\*. .\* \*\*\* .\*\*.. . \* \*\* \*.\* \*...\*\*\*\*\*.\*\*... \* . \*

HR VHDSADFYIEFAKMCKYANNSLVTVGVFISFTISFFLSRLVILPLWIVPSIWFGIYTYN

HP AFFGYFFNSMMGVLQLLHIFWAYLILRMAHKFITGKLVEDERSDREETESSEGEAAAAG

10 .. ..\* ... .\*\*\*\*\*.\* \*.. \*. \* ..\* . . .\*.\*.\*.\*. \* .

HR CAMA-WLFCALL-ILQLLHFYWF SHIVKAAYASILVGVIERDTRSESEDSSAEDETAKYS

HP GGAKSRLPLANGHPILNNNHRKND

\*,

15 HR VGSGDYTESNGIHKRVVTAR

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The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
20 sequences that shared a homology of 90% or more (for example,  
Accession No. T27334) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they

25 <HP03499> (SEQ ID NOS: 5, 15 and 25)

Determination of the whole base sequence of the cDNA insert of clone HP03499 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 1758-bp ORF, and a 86-bp 3'-untranslated region. The ORF encodes a protein consisting of 585 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 63 kDa that was almost identical with the molecular weight of 63,987 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 82 kDa. In addition, there exist in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 89, Asn-Glu-Thr at position 106, Asn-Ala-Thr at position 189, Asn-Arg-Thr at position 220 and Asn-Ala-Thr at position 315).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Chinese hamster hypothetical protein 2BE2121 (Accession No. A30227). Table 7 shows the hypothetical protein 2BE2121 (CH). Therein, the marks of -,

\*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a  
5 homology of 44.8% in the entire region.

Table 7

```

HP  MVCREQLSKNQVKWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG
10                                     ..***.*.

CH                                     SWSENILDYFLRNS

HP  QISRRDALEVWYHAANSKKAMTAALNSNITVLEADVNEGLGTANETGVPIMAHPTIY
    **.  *.  *..***** *.  *  **.  *  ..**** . .  ...* * *****,.
15 CH  QITTEDGAEIIWYHAANHKSQMQEALRSAAHMIEADVLLPS--DGSEHGQPIMAHPPEN
    *****..**.*.  *.*****.. *.  *.  *  ....  .. *.  *.  *.  *  **

CH  SDNTLQEWLAEVM-KSNKGIKLDFKSLAAARASMLFLDNVKQH--LQCPVWMNADVLPGP
20                                     *****..**.*.  *.*****.. *.  *.  *  ....  .. *.  *.  *.  *  **

HP  NMLISTEVNATQFLALVQEKYPKATLSPGWTTFYMSTSPNRTYTQAMVEKMHELVGVPQ
    *  *.  *.  *.  **.  *  .  *.  *.  *  **** . . .  *  *.  **.  *.  .  *.  *

CH  NG-SSKVVDAKAEIDVTSEPPDYTESLQWTTGWDEKVNDEGVSWTMYKEMDYGGLTO
25 HP  RVTEFPVRSSMVRAAWPHFSWLLSQSERYSLTLWQAASDPMSVEDLLYVRDNTAVHQVYYD

```

.\*\*\*\*\*...\*\*.. ... \*\*\*..\*.\*\*\*\*\*.\* . .\*. ..\*\*\*\*\*.\*\* . \*\*.\*\*

CH PVTFPVRAALVRQSCSQLLWLLKKSNNRYSLTVWTGKDDSYPTEDLLYIRDYFNKTQVFYD

HP IFEPLLSQFKQLALNATRKPMYYTGGSLIPLLQLPGDDGLNVEWLVPDVQGSgKTATMTL

5       \*.\*\* .\*\*\*

CH ILEPQSHEFKQAIGI

Furthermore, the search of the GenBank using the  
 10 base sequences of the present cDNA has revealed the  
 registration of sequences that shared a homology of 90% or  
 more (for example, Accession No. R92398) among ESTs. However,  
 since they are partial sequences, it can not be judged  
 whether or not they encode the same protein as the protein  
 15 of the present invention.

<HP03500> (SEQ ID NOS: 6, 16 and 26)

Determination of the whole base sequence of the  
 cDNA insert of clone HP03500 obtained from cDNA library of  
 human kidney revealed the structure consisting of a 134-bp  
 20 5'-untranslated region, a 996-bp ORF, and a 476-bp 3'-  
 untranslated region. The ORF encodes a protein consisting of  
 331 amino acid residues and there existed one putative

25 Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 37,694 predicted from the ORF.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the amino acid sequence of the protein matched with that of human hypothetical protein (Accession No. AAC05803) in which a region of 62 amino acid residues from glycine at position 88 to lysine at position 149 was deleted.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340631) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
15 encode the same protein as the protein of the present invention.

<HP10691> (SEQ ID NOS: 7, 17 and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10691 obtained from cDNA library of  
20 human umbilical cord blood revealed the structure consisting of a 246-bp 5'-untranslated region, a 1038-bp ORF, and a 1096-bp 3'-untranslated region. The ORF encodes a protein

25 the hydrophobicity/hydrophilicity profile, obtained by the

Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human BB1 protein (Accession No. AAB37433). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human BB1 protein (BB). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The C-terminal region of 215 amino acid residues of the present protein shared a homology of 81.9% with the N-terminal region of human BB1 protein.

Table 8

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HP	MSPEEWTYLVVLLISIPICFLFKAGPGLKRWGAAVGLGLTLFTCGPHTLHSLVTILGT
HP	WALIQAQPCSCHALALAWTFSYLLFFRALSLLGLPTPTPFTNAVQLLLTLKLVSLASEVQ
BB	MASGFSKGPTLGLLRRALPDGDT-QLQLLLRGNHDRPVLPPLPGLAGAA

HP FPGAVPSLRPLLRRWPAPLFGLLFLLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

. \* . .\*\*\*\*\*

BB LPRGSASLRPLLRRWPAPLFGLLFLLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

5

HP FRMRFYVAWIAAECGCIAAGFGAYPVA AKARAGGGPTLQCPPSSPEKAASLEYDYETIR

\*\*\*\*\*

BB FRMRFYVAWIAAECGCIAAGFGAYPVA AKARAGGGPTLQCPPSSPEKAASLEYDYETIR

10

HP NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRL

\*\*\*\*\*

BB NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRTAWTMLSAYWHGLHP

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W48653) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

<HP10703> (SEQ ID NOS: 8, 18 and 28)

Determination of the whole base sequence of the

25

human kidney revealed the structure consisting of a 359-bp

5'-untranslated region, a 270-bp ORF, and a 1388-bp 3'-untranslated region. The ORF encodes a protein consisting of 89 amino acid residues and there existed one putative transmembrane domain. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18 kDa that was larger than the molecular weight of 10,469 predicted from the ORF.

10           The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T08343) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10711> (SEQ ID NOS: 9, 19 and 29)

20           Determination of the whole base sequence of the cDNA insert of clone HP10711 obtained from cDNA library of human kidney revealed the structure consisting of a 29-bp 5'-untranslated region, a 1221-bp ORF, and a 356-bp 3'-untranslated region. The ORF encodes a protein consisting of  
25           transmembrane domain at the N-terminus. Figure 9 depicts the



hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 44 kDa that was almost identical with the molecular weight of 43,836 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Ser-Thr at position 65, Asn-Trp-Ser at position 95, Asn-Val-Ser at position 134, Asn-Ile-Thr at position 159, Asn-Gly-Ser at position 187, Asn-Arg-Ser at position 230 and Asn-Leu-Thr at position 333). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 36.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse kidney predominant protein (Accession No. BAA92527). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse kidney predominant protein (MM). Therein, the marks of -, \*, and . represent a gap, an

of the protein of the present invention, respectively. The

both proteins shared a homology of 79.9% in the entire region.

Table 9

5

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HS MRGSVECTWGWGHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIR

\* \*\*\* .\*\*\*.\* \*\* .\*\* .\*\*\*\*\* \*\*.\*\*\*\*\*.\*\*\*.\* \* \*\*\*\*\*

MM MFRCWGPHWGWVPCAPTPWLLLSLLVCSAPFGLQGEETRQVSMEVISGWPNP-QNLLHIR

10

HS AVGTNSTLHYVWSSLGPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSS

\*\*\*.\*\*\*\*\*.\*\*\*.\*\*\*\*\*.\*.\*\*\*\*\*.\*\*\*.\*\*\*.\*\*\*\*\*.\*\*\*\*\*

MM AVGSNSTLHYVWSSLGPPAVVLVATNTTQSVLSVNWSLLLSLDPAGALMVLPKSSIQFSS

15

HS ALVFTRLLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMND

\*\*\*\*\*.\*\*\*.\*.\*.\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*.\*.\*\*\*.\*\*\*.\*.\*

MM ALVFTRLLEFDSTNASE-GAQQPGKPYPPYSLAKFSWNNITNSLDLANLSADFQGRPVDD

HS PTRTFANGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVAT

\*\* .\*\*\*\*\*.\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*

20

MM PTGAFANGSLTFKVQAFSRSGRPAQPPRLLHTADVCQLEVALVGASPRGNIISLFGLEVAT

HS LGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSIPSGFAQWRPVAYSQKPGGRESALPC

\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*

25

MM QASTLHSTLASSLPHSPIVQAFFGSQNNFCAFNLTFGAPTGPQYWDQYYLCWSMLLGMGF

\*\*\*\*\* , \*\*\*\*\* , \*\*\*\*\* \*\*\*\*\*, \*, , \*\*\*\*\*

MM PPVDIFSPLVLGIMAVALGAPGLMFLGGGLFLLLRRHRYSEYQSIIN

<HP10712> (SEQ ID NOS: 10, 20 and 30)

25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse calcium channel gamma 5 subunit (Accession No. CAB86387). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse calcium channel gamma 5 subunit (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 75.0% in the entire region.

Table 10

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HS MTAVGVQAQRPLGQRQPRRSFFESFIRTLIITCVALAVVLSSVSICDGHWLLAEDRLFGL

20       \*\*\*.\*.\*\*.. \*\* ..\*.\*\*\*\*\*. \*.\*\*\*\*\*. \*\*, \*\*\*\*

MM MTAIGAQAHLKLLGLKRPHRSFFESFIRTLIIVCTALAVVLSSVSICDGHWLLVEDHLFGL

HS WHFCTTTNQSVPICFRDLGQAHPGLAVGMGLVRSVGALAVVAATFGLFELMVSQLCEDK

MM WHFCTTTNQSVPICFRDLGQAHPGLAVGMGLVRSVGALAVVAATFGLFELMVSQLCEDK

HS HSQCKWVMGSILLVSVFLSSGGLLGFVILLRNQVTLIGFTLMFWCEFTASFLFLNAIS

. \*. \*\*. \*\* \*\*\*\*. \*. \*\*\*\*. \*. \*\*. \*. \*. \*\*\*\*. \*\*\*\* \*

MM RSRRKWAIGSYLLLVAFILSSGGLLTFIILLKNQINLLGFTLMFWCEFTASFLFLNAAS

5

HS GLHINSITHPWE

\*\*\*\*. \*. \*\*.

MM GLHINSLTQPWDPPAGTLAYRKRGYDGTSLI

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA910339) among ESTs.

15 However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03010> (SEQ ID NOS: 31, 41 and 51)

20 Determination of the whole base sequence of the cDNA insert of clone HP03010 obtained from cDNA library of human kidney revealed the structure consisting of a 97-bp 5'-untranslated region, a 1134-bp ORF, and a 320-bp 3'-untranslated region.

25 putative transmembrane domains. Figure 11 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was almost identical with the molecular weight of 41,462 predicted from the ORF as well as a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* hypothetical protein (Accession No. AAC34490). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* hypothetical protein (AT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 42.0% in the entire region other than the N-terminal region.

Table 11

---

HP MDSALSDPHNGSAFACGPTNSTTRPPSTDEGLALAVGSLLMALLDIEGALDSVPGAGC

AT MKNCERFANLALAGLTLAPLVVRVNPNLNVILTACITVYVGCFRS

HP KNASDMPETITSRDAARFPIIASCTLLGLYLFFKIFSQEYINLLLSMYFFVLGILALSH

. . . , \*\* . . . \* \*\*\*\* . . . \* \*\*, \*, \*. \*\*, . \*, . . , \* , \*, \*\*\*\*\* \*\*\*\* \*

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AT VKDTPPTETMSKEHAMRFPLVGSAMLLSLFLFKFLSKDLVNAVLTAYFFVLGIVALSAT

5

HP ISPFMNKFFPASFPNRQYQLLFTQGSGENKEEIINYEFDTKDLVCLGLSSIVGVWYLLRK

. \* . . . \* \* . . . . \* . . . \*\* . . . . \* . . . . \*\* . \*

AT LLPAIRRF L PNPW N D N L I V W R F-----PYFKSLEVEFTKSQV VAGIPGTFFCAWYAWKK

10 HP HWIANNLFLGLAFSLNGVELLHLNNVSTGCILLGGFLFYDVFVWFGTNVMVTVAKSFEAPI

\*\*\*.\*\*\*. \*\*. \*. . \*. \*. \* \*. . . \*\* \*\*\*.\*\*\*.\*\*\*.\*\*\*.\*\*\* \* \*\*\*.\*\*\*.\*\*\*.\*\*\*

AT HWLANNILGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDAP

HP KLVFPQDLLEKGLEANNFAMGLGDVVIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF

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15      **, ** .      . . * .      . . *****. *****. ** *****. * . . . . . ** . . * . *
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AT KLLFPTG---DALRP--YSMLGLGDIVIPGIFVALALRFDVSRRRQPQ-YFTSAFIGYAV

HP GLGLTIFIMHIFKHAQPALLYLPACIGFPVLVALAKGEVTEMFSEESNPKDPAAVTES

\*. \*\*\*. \*. \*. \*\*\*\*\*. \*\*\*\*. \*\*\*\*. . \*. . . . . \*\*. . . . \*. . . \*\*

20 AT GVILTIVVNWFWAAQPALLYIVPAVIGFLASHCIWNGDIKPLLAFFDESKTEE-ATTDES

HP KEGTEASASKGLEKKEK

\* \*

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA380429) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03576> (SEQ ID NOS: 32, 42 and 52)

Determination of the whole base sequence of the cDNA insert of clone HP03576 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 246-bp ORF, and a 1379-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed two putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 9,178 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein (HP03576) revealed that it was identical to the protein of human kidney (Accession No. NP\_003936).

Table 12 shows the comparison



between amino acid sequences of the human protein of the present invention (HP) and human vacuolar proton ATPase 9 kDa (VP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 71.2% in the entire region.

Table 12

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HP MTAHSFALPVIIFTTFWGLVGIAGPWFVPKGPNRGVIIITMLVATAVCCYLFWLIAILAQL

\*. \*. ... \*. \*. ... \*\*\*. \*\*. \*\*\*. \*\*\*\*\*. . \*\*\*\*\*

VP MAYHGLTVPLIVMSVFWGFGFLVPWFIPKGPNRGVIIITMLVTCSVCCYLFWLIAILAQL

HP NPLFGPQLKNETIWYVRFLWE

\*\*\*\*\*... \*

VP NPLFGPQLKNETIWYLKYHWP

---

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that are identical to the present cDNA.

since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein of the present invention.

<HP03611> (SEQ ID NOS: 33, 43 and 53)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP03611 obtained from cDNA library of  
human kidney revealed the structure consisting of a 189-bp  
5'-untranslated region, a 1464-bp ORF, and a 105-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
10 transmembrane domains. Figure 13 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of high molecular weight.

15 The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to human cystine/glutamate transporter  
(Accession No. BAA82628). Table 13 shows the comparison  
between amino acid sequences of the human protein of the  
20 present invention (HP) and human cystine/glutamate  
transporter (CG). Therein, the marks of -, \*, and .  
represent a gap, an amino acid residue identical with that  
of the protein of the present invention, and an amino acid  
25 invention, respectively. The both proteins shared a homology

of 43.8% in the entire region other than the N-terminal region.

Table 13

5

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HP MGD TGLRKRREDEKSIQSQEPKTTSLQKELGLISGISIIVGTIIGS

..... \*. .... \*. .... \*. .... \*. .... \*

CG MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRKVTLLRGVSIIGTIIGA

10

HP GIFVSPKSVLSNTEAVGPCLIIWAACGVLATLGALCFELGTMITKSGGEYPYLMEAYGP

\*\*\*. \*\*\*. \*\* \*\* . \*\* . \*. \*\* . \*\*\*\*\*. .... \*. \*\*\*\*\* \*. \*\*\*\*\*. \*. \*. . \*\*

CG GIFISPKGVLQNTGSGVMSLTIWTVCGVLSLFGALSYAELGTTIKKSGGHYTYILEVFGP

HP IPAYLFSWASLIVIKPTSFATIIICLSFSEYVCAPFYVGCKPPQIVVKLAAAAILFISTVN

15

. \*\* . . \*. \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \*

CG LPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEIPELAIKLITAVGITVVMVLN

HP SLSVRLGSYVQNIFTAAKLIVIVAIISGLVLLAQGNTKNFDNSFEGAQLSVGAISLAFY

\*. \*. . . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \*

20

CG SMSVSWSARIQIFLTFCKLTAILIIIVPGVMQLIKGQTQNFKDAFSGRDSSITRLPLAFY

HP NGLWAYDGWNQLNYITEELRNPNYRNPLAIIIGIPLVTACYILMNVSYFTVMTATELLQS

\* \*

25

HP QAVAVTFGDRVLYPASWIVPLFVAFSTIGAANGTCFTAGRLIYVAGREGHMLKVLSYISV

.\*\*\*\*\*.\*.\* \* \*\*.\*\*\*.\*.\* \*\*.\*...\*\*.\*\*\*.\*\*\*.\*..\*\*.\*

CG NAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV

5 HP RRLTPAPAIIFYGIIATIIYIIPGDINSLVNYFSFAAWLFYGLTILGLIVMRFRKELERP

\*. \*\*.\*.\* .. \* ...\*\*.\*\*\*.\*...\*\*\* \*\*.\*\*\*.\*...\*\*\*.\*.. ...\*\*

CG RKHTPLPAVIVLHPLTMIMLFSGDLDLLNFLSFARWLFIGLAVAGLIYLRKCPDMHRP

HP IKVPVVIPVLMTLISVFLVLAPIISKPTWEYLYCVLFILSGLLFYFLFVHY--KFGWAQK

10 .\*\*\*. \*\*.\*.....\*.\* .. \*.\*.. ...\*.\* \*.\*.\*. \*.\*. \*.\*.

CG FKVPLFIPALFSFTCLFMVALSLYSDP-FSTGIGFVITLTGVPAYYLFIIWDKKPRWFRI

HP ISKPITMHLQMLMEVVPPEEDPE

.\*. \*\*. \*\*...\*\*\*\*\* \*.

15 CG MSEKITRTLQIILEVVPPEEDKL

20 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R07056) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

Determination of the whole base sequence of the cDNA insert of clone HP03612 obtained from cDNA library of human kidney revealed the structure consisting of a 153-bp 5'-untranslated region, a 1128-bp ORF, and a 269-bp 3'-untranslated region. The ORF encodes a protein consisting of 375 amino acid residues and there existed seven putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 39 kDa that was somewhat larger than the molecular weight of 37,930 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human monocarboxylate transporter (Accession No. AAC70919). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human monocarboxylate transporter (MC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.26% at the amino acid



HP DDADEPRGAPGPSPVRLPKG

MC TLMDLVGAPRFSSAVGLVTIVECGPVLLGPPLAGKLVDLTGEYKMYMSCGAIVVAASVW

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI742291) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10407> (SEQ ID NOS: 35, 45 and 55)

15 Determination of the whole base sequence of the cDNA insert of clone HP10407 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 100-bp 5'-untranslated region, a 1053-bp ORF, and a 332-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed at least four putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 acid sequence of the present protein revealed that the

protein was longer by 35 amino acid residues at the N-terminus than human hypothetical protein (Accession No. CAB43375).

Furthermore, the search of the GenBank using the  
5 base sequences of the present cDNA has revealed the registration of a clone beginning from the 117th base of the present cDNA (Accession No. AL050274).

<HP10713> (SEQ ID NOS: 36, 46 and 56)

Determination of the whole base sequence of the  
10 cDNA insert of clone HP10713 obtained from cDNA library of human kidney revealed the structure consisting of a 79-bp 5'-untranslated region, a 2004-bp ORF, and a 611-bp 3'-untranslated region. The ORF encodes a protein consisting of  
15 667 amino acid residues and there existed nine putative transmembrane domains. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse retinoic acid-responsive protein (Accession No. U01601).

25 of the present invention (HP) and mouse retinoic acid-



responsive protein (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.1% in the entire region.

Table 15

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10 HP MSSQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLAS  
 \*.\*\*\*.\*.\*.\*\*\* \*\*\*\*.\*.\*\*\*.\*\*\*\*.\*.\*. . \*\*.\* \*\*\*\*.\*  
 MM MESQASENGSQTSSGVTDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLAS

HP LSILVLLLLAMLVRRRQLWPDCVRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL  
 15 \*\*.\*\*\*\*.\*.\*\*\*\*.\*.\*\*\* \* . \*\*\*\*\* ..\*\*\*\*.\*.\*.\*\*\*\*.\*  
 MM LSFLVLLLLALLVRRRRLWPRCGHRGLPLSPVDFLAGDLSWTVPAAVFVVLFSNLCLLL

HP PDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFYAAALYYPLAACATAGHTAAHLLGST  
 \*\*.\*.\*\*\*\*.\*.\*.\*.\*. \*.\*.\*\*\*.\*.\*.\*.\*\*\*\*\*.\*\*\* \*\* \*\*.\*.  
 20 MM PDENPLPFLNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAALLGTV

HP LSWAHLGVQVWQRAECPQVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG

HP SKGLQSSYSEEYLRNLLCRKKLGSSYH-TSKHGFLSWARVCLRHCIYTPQPGFHLPLKLV

\*.\*\*\*.\*\*\*\*.\*\*\*.\*\*\*.\*\*\*.\*. \* ,\*\*.,.,\*\*.\*.,. .\*,\*\*\*\*\*.\*\*\*\*\*

MM SQGLQTSYSEKYLRTLLCPKKLDSCSHPAKRSLLSRAWAFSHHSIYTPQPGFRLPLKLV

5 HP LSATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVELVKH

, \*\*\*\*\*, \*\*\*\*\*\*, \*\*, \*\*\*\*\*., , \*\*\*\*\*, \*\*\*\*\*

MM ISATLTGTATYQVALLLVSVVPTVQKVRAGINTDVSYLLAGFGIVLSEDRQEVVELVKH

HP HLWALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI

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10      ***. *.*****      ***. *.***      ***. **.*****. *      . * *****
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MM HLWTVEACYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPLQSIHPSRQAI

HP FCWMSFSAYQTAFICLGLLVQQIIFFLGTTALAFVLMPVLHGRNLLLFRSLESSWPFWL

\*\*\*\*\*

15 MM VSWMSFCAYQTAFSCLGLLVQQVIFFLGTTSLAFLVFVPLLHGRNLLLSLESTWPFWL

HP TLALAVILQNMAAHWVFLETHDGHQPQLNRRVLYAATFLLFPLNVLVGAMVATWRVLLSA

\*.\*\*\*\*\*.\*\*,\*.\*\* \*\*\*,\*.\*.\*\*\*\*\*,\*.,\*\*\*\*\*,\*.,\*\*\*\*\*,\*.

MM TVALAVILQNI AANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISS

20

HP LYNAIHLGQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPMATAFCSLLLQAQSLLPR

\*\*\* \*\*\*\*\* \*\*\*\* \*\*\*\*\* \*\* \*\*\* \*\* \*\*\*\*\* , , \*\*\*\* , \*\*, \* \* \*\*

100. LANTYU COMD CUI DORASI DDVITYOMI DE FACCHOMI ANCAI LILADONEND

25

HP TMAAPQDSLRLPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTL LHNPTLQVFRKT

. \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* . \*. \*\*\*\*\* \*\* \*\*.

MM PPLAPQDSLPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKA

HP ALLGANGAQP

5        \*\* \*. .

MM ALTSAKANGTQP

10        The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. AI760170) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
15        encode the same protein as the protein of the present  
invention.

<HP10714> (SEQ ID NOS: 37, 47 and 57)

20        Determination of the whole base sequence of the  
cDNA insert of clone HP10714 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 82-bp 5'-untranslated region, a 1395-bp ORF, and a  
1820-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 464 amino acid residues and there existed a  
putative secretory signal at the N-terminus. This was  
25        by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 49 kDa that was somewhat smaller than the molecular weight of 52,340 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 52 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 164 and Asn-Asp-Ser at position 320). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from threonine at position 22.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA861134) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10716> (SEQ ID NOS: 38, 48 and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10716 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 60 bp 5' untranslated region, a 1412 bp ORF, and a 252 bp 3' untranslated region. The ORF encodes a protein consisting of 470 amino acid residues and there existed one

putative transmembrane domain at the N-terminus. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was larger than the molecular weight of 52,086 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-90 (Accession No. AAD34085). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-90 (CG). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the entire region.

Table 16

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HP MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG

HP EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTTAN

CG

MALAARLWRLLPFRRGAAPGSRLPA

5 HP AESDNERDSKESEDGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGGSSGLEDVLP

\* \* \*

CG GPSGSRGIAAPARFRGFVEMGNPGTFNRGLLSALS YLGFETYQVISQAAVVHATAKVEE

HP LLQQADELHRGDEQGKREGFQLLLNNKLVYGSRQDFLWRLARAYSDMCELT-EEVSEKKS

```
10      .*.*** *. ..* .*      .*** . *      .. ...***** .*. *. .. .***
```

CG ILEQADYLYESGETEK--LYQLLTQYK--ESEDAELLWRLARASRDVAQLSRTSEEEKKL

HP YALDGKEEAEEALEKGDDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQ

..... \* \*. \*\*\*\*\*..... \* .. \* \*\*\*\*..... ..... \*. \*. ..... \*. ..... \*\*\*\*\* ..... \*\*\*\*. \*.

15 CG LVYEALEYAKRALEKNESSFASHKWYAICLSVDYEGIKAKIANAYIIKEHFKAIELN

HP PENPMAHFLLGRCYQVSHLSWLEKKTATALLSPLSATVEDALQSFLKAEELQPGFSKA

\* . . . \* \* \*\* \* . . . \* . . . \* \* . . . \*

CG PKDATSIHLMGIWCYTFAEMPWYQRRIAKMLFATPPSSTYEKALGYFHRAEQVDPNFYSK

20

HP GRVYISKCYRELGKNSEARWWMKLALELPDVTKEDLAIQKDLEELEVLIRD

. . . \* \* , \* . . . \* , \* , \* , \* , \* , \*\* , \*\* , . . . \* . . .

— **ВНЕШНЕ-ЭКОНОМИЧЕСКАЯ ПОЛИТИКА И МЕЖДУНАРОДНЫЕ ОТНОШЕНИЯ**

25

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA852295) among ESTs. However, since they are  
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10717> (SEQ ID NOS: 39, 49 and 59)

Determination of the whole base sequence of the  
10 cDNA insert of clone HP10717 obtained from cDNA library of human kidney revealed the structure consisting of a 73-bp 5'-untranslated region, a 732-bp ORF, and a 976-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed two putative  
15 transmembrane domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was larger than the molecular weight of  
20 26,270 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of  
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10718> (SEQ ID NOS: 40, 50 and 60)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP10718 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 86-bp 5'-untranslated region, a 813-bp ORF, and a 889-  
bp 3'-untranslated region. The ORF encodes a protein  
consisting of 270 amino acid residues and there existed  
10 three putative transmembrane domains. Figure 20 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 28 kDa that was smaller than the molecular weight of  
15 31,116 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein Y53C10A (Accession No. CAA22139). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein Y53C10A (CE). Therein, the marks of -, amino acid residue similar to that of the protein of the



present invention, respectively. The both proteins shared a homology of 54.8% in the entire region other than the N-terminal region.

## 5 Table 17

HP

MAGAEDWPGQ

CE MTSSSAASSSTTTSTMPDENELCKKEEERFKSPDPAPTLDEEVDIDTLPSMLEDDPNG

10

HP QLELDEDEASCCRWGAQHAGARELAALYSPGKRLQEWCSVILCFSLIAHNLVHLLLLARW

\*\*\*.\*\*\*\*\*.\*\*\*.\*\*\*.\*\*\*\*\* \*.. . \*.. ... \*\*\*. \*

CE NVVECDLGFKGPRWGPQHAGAKKLASMYSKEKRLQEKVSLFAAIFLFSIVFIN-LLLS-W

15

HP EDT--PLVILGVVAGALIADFLSGLVHWGADTWGSVELPIVGKAFIRPFREHHIDPTAIT

\*.. \*... \* \* ..\*\*\* \*\*\*\*\*.\*\*\*.\*\*\*\*. \*..\*\*\*\*\*.\*\*\*\*\*

CE ESSIWVSVLVSAVLGIMTADFASGLVHWAADTFGSVE-TWFGRSFIRPFREHHVDPTAIT

HP RHDFIETNGDNCLVTLLPLLNMAYKFRTHSPEALEQ--LYPWECFVFCIIIFGTFTNQIH

20

\*\*\*.\*.\*\*\*\*\*.. \*\*\*. \*. \*. ..\*..\* ..\* ... \* \*. ..\*\*\*\*\*

CE RHDIVEVNGDNCLCVGPLLWILYQQMTYQRDAITQWATFW--YILLGGIYVALTNQIH

25

CE KWSHTYFGLPTWVVFLLQKAHIILPRSHHKIHHISPHACYYCITTGWLNPLEYIGFWRKM

HP EDLIQGLTGEKPRADDMKWAQKIK

\* . . . \*\* . \*\* . \*\* . \*\* \*

CE EWVVTTVTGMQPREDDLKWATKLQ

5

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA176107) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, the region from position 466 to position 778 of the cDNA of the present invention matched with the region from position 2 to position 314 of human ubiquitin-conjugating enzyme E2 variant 1 (Accession NO. NM\_003349) although no match was observed in another region.

<HP03745> (SEQ ID NOS: 61, 71 and 81)

20 Determination of the whole base sequence of the cDNA insert of clone HP03745 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp

25 389 amino acid residues and there existed at least nine

putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 7 (Accession No. NP\_003974). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 7 (SC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.0% in the N-terminal region of 397 amino acid residues.

Table 18

20

HP

MDRGEKIQLKRVFGYWWGTSFLLINIIG

.\*.\*\*\*. .. \*.\*... \*.\*\*

25

HP AGIFVSPKGVLAYSCMNVGVSLCVWAGCAILAMTSTLCSAEISISFPCSGAQYYFLKRYF

.\*\*\*\*\*... . \*.\*\* \*\*\* .....\*\* \*\*..... \*\*\* \* .. \*

SC SGIFVSPKGVLVHT-ASYGMSLIVWAIGGLFSVVGALCYAELGTTITKSGASYAYILEAF

HP GSTVAFNLWTSFLGSGVVAG-QALLAEYSIQPFPSVVKLPKKCLALAMLWIVGI

5       \*. \*\*.\*\*.\*\*. . . . . \*. \*\*. \* \*\*\* \*\*\*\*. \* \*. . \*\* \* . ....

SC GGFIAFIRLWVSLLVVEPTGQAIITFANYIIQPSFPSCDPPYLACRLAAACICLLTF

HP LTRGVKEVTWLQIASSVLKVSILSFISLTGVVFLIRGKKENVERFQNAFDAELPDISHL

      ... \*\* \*.\*. . . \*\* \* \* . \*. \* \* . \* . \*.\*\*.\*. . \*.\*\*

10       SC VNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQG--HSEHFQDAFEGSSWDMGNL

HP IQAIFQGYFAYSG-----ELKKPRTTIPKCIFTALPLVTVVYLLVNISYLTVLTPR

      \*. . \*.\*\*\*       \*. \* \* . \* \* . . \*.\*\*.\*. \*.\*\*.\* \*\*\*. .

SC SLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMPIVTLIYILTNVAYYTVLNIS

15       HP EILSSDAVAITWADRAFP SLAWIMPFAISTSLFSNLLISIFKSSRPIYLASQEGQLPLLF

      ..\*\*\*\*\*. \*.\*\*.\* . .\*.\*.\*. \* \*.\*\* \*\*\* \*\*\*\* . . . \*.\*\*.\* \*.

SC DVLSSDAVAVTFADQTFGMFSWTIPIAVALSCFGGLNASIFASSRLFFVGSREGHLPDLL

20       HP NTLNSHS-SPFTAVLLLVTLGSLAIILTSLIDLINIFYFTGSLWSILLMIGILRRRYQEP

      . . . . \*.\*\*.\*. \*. . . \*. . . . \*\*\*\*. \*. . . \* . \* \* \*.\*\*

SC SMIHIERFTPIPALLFNCTMALIYLVEDVFQLINIFYFSFSYFFFVGLSVVGQLYLRWKEP

25       . . \* \* . . \*

SC KRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTINSLIGIGIALSGVPPFYFMGVYLPESRR

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<HP03747> (SEQ ID NOS: 62, 72 and 82)

5           Determination of the whole base sequence of the  
cDNA insert of clone HP03747 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 21-bp 5'-untranslated region, a 1047-bp ORF, and a  
1324-bp 3'-untranslated region. The ORF encodes a protein  
10       consisting of 348 amino acid residues and there existed a  
putative secretory signal at the N-terminus and one putative  
transmembrane domain at the C-terminus. Figure 22 depicts  
the hydrophobicity/hydrophilicity profile, obtained by the  
Kyte-Doolittle method, of the present protein. In vitro  
15       translation resulted in formation of a translation product  
of 40 kDa that was almost identical with the molecular  
weight of 39,685 predicted from the ORF. Application of the  
(-3,-1) rule, a method for predicting the cleavage site of  
the secretory signal sequence, allows to expect that the  
20       mature protein starts from proline at position 39.

          The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
  
25       comparison between amino acid sequences of the human protein

of the present invention (HP) and human endoplasmic reticulum glycoprotein (ER). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.1% in the entire region.

Table 19

HP MAATLGPLGSWQ-QW-RRCLSARD-----GSRMLLLLLLLGSGQGPQQVGAGQTFEYLK

\*. \* \*\*\*\*. .. \*. \*. \*\*\*\*\* \* . . . . . \*. \*. \*\*

ER MAAEGWIWRWGWGRRCLGRPGLLGPGPGPTTPLFLLLL-LGSVTADITDGNS-EHLK

15 HP REHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQ

\*\*\*\*\* \*\*\*\*\* . \* . \*\* . \* . \* . \*\* . \*\*\*\*\* . \*\* . \* . \*\* . \*\*\*\*\* . \*\*\*\* .

ER REHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVRLTPDERSKEGSIWNHQPCFLKDWEMH

HP VHFKIHGQGKKNLHGDGLAIWYTKDRMQPGPVFGNMDK FVGLGVFVD TYPNEEKQQERVF

\*\*\*\*\* \*\* \*\*\*\*\*\*\*\*\*\* \* \*\*\*\*\* \*\* \*\*\*\*\*\*\*\*\*\* \* \*\*\*\*\*

ER VHFKVHGTGKKNLHGDGIALWYTRDRLVPGPVFGSKDNFHGLAIFLDTYPNDET-TERVF

UD 0013455001 CYRILPOCOTTE 10 07 1994 11 07 1994 11 07 1994

25 ER PYISVMVNGSLSYDHSKDGRWTELAGCTADFRNRDHDTEFLAVRYSRGRLTVMTDLEDKN

HP EWRDCIEVPGVRLPRGYFFGTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLP

\*\*..\*\*...\*\*\*\*\* \*\*\*,\*. \*\*\*\*\*.\*\*, \*\*\*,\* \*\*\*,\*\*.,.... . \*

ER EWKNCIDITGVRLPTGYFFGASAGTGDLSNHDIIISMKLFQLMVEHTPDEESIDWTKIEP

5

HP SVDNMKLP-----EMTAPL--PPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQRK

\*\*..\* \* . \*. . \*\*.\* .\*\*,... \*. \* \*. \* ....\*,\*\*.. \*

ER SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLLCALLGIVVCAVVGAVVFQKRQERN-K

10

HP RFY

\*\*\*

ER RFY

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA262924) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

<HP10719> (SEQ ID NOS: 63, 73 and 83)

25

human kidney revealed the structure consisting of a 54-bp

5'-untranslated region, a 786-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 261 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was larger than the molecular weight of 27,435 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from asparagine at position 19.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse endomucin (Accession No. AAD05208). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse endomucin (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present



Table 20

---

HP MELLQVTIL-FLLP-SIC-SSNSTGVL-EAANNSLVVTTTKPSITTPNTESLQKNVVTPT

\* \*\*\*,\*. \* \*\*\*, \*. \* \*. ....\* .. .. ..\*\*\*,\*. \*. \*. \* ..\* ..\* ..\*

5 MM MRLLQATVLFLLSNSLCHSEDGKDVQNDSIPTPAETSTTKASVTIPGIVSV-TNPNKPA

HP TGTPKGTITNELLKMSLMSTATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPLNAV

..\*\*,\*.\*. .... . \*\*..\* . \*\*. .... .\*\*.. ..\*.\* . ..\*\*.. .... .\*\*

MM DGTPPEGTTKSDVSQTSLVTTINSLTTPKHEVGTTTEGPLRNESSMTKITVPNTPTSAN

10

HP STLQSSPKKTETQSSIKTTEIPGSVLQPDASPKTGTLTSPVTIPENTSQSQVIGTEGG

\*\*\*,\*. \*.\*\* .. . .\*.\*\* .. . . \* ..\*\*.

MM STLPGSQNKITTQ-----LLDALPKITATPS-----ASLTTAHTMSLLQDTEDR

15

HP KNASTSATRSYSSIILPVVIALIVITLSVFVLVGLYRMCWKADPGTPENGNDQPQSDKE

\* \*,\*..\*..\*\*\*\*\*. \*\*\*\* \*\*,\*\*\*\*\*. \*\*\* \*\*\*\*\*

MM KIATTPSTTPSYSSIILPVVIALVVITLLVFTLVGLYRICWKRDPGTPENGNDQPQSDKE

HP SVKLLTVKTISHESGEHSAQGKTKN

20

\*\*\*\*\*

MM SVKLLTVKTISHESGEHSAQGKTKN

---

25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AA486620) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10720> (SEQ ID NOS: 64, 74 and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10720 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 669-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 222 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,219 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 35 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-  
cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from glutamic acid at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792241) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10721> (SEQ ID NOS: 65, 75 and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10721 obtained from cDNA library of human kidney revealed the structure consisting of a 74-bp 5'-untranslated region, a 552-bp ORF, and a 1658-bp 3'-untranslated region. The ORF encodes a protein consisting of 183 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight

Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 25.

The search of the GenBank using the base sequences  
5 of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R27187) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present  
10 invention.

<HP10725> (SEQ ID NOS: 66, 76 and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10725 obtained from cDNA library of human kidney revealed the structure consisting of a 235-bp  
15 5'-untranslated region, a 789-bp ORF, and a 713-bp 3'-untranslated region. The ORF encodes a protein consisting of 262 amino acid residues and there existed one putative transmembrane domain. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro  
20 translation resulted in formation of a translation product of high molecular weight.

25 sequences that shared a homology of 90% or more (for example,

Accession No. AI127782) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5                   <HP10727> (SEQ ID NOS: 67, 77 and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10727 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 102-bp 5'-untranslated region, a 507-bp ORF, and a 947-  
10 bp 3'-untranslated region. The ORF encodes a protein consisting of 168 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the  
15 Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was larger than the molecular weight of 17,822 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa.  
20 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at  
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. R80316) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10728> (SEQ ID NOS: 68, 78 and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10728 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 221-bp 5'-untranslated region, a 732-bp ORF, and a 902-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 26,534 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H23535) among ESTs. However, since they are invention.

<HP10730> (SEQ ID NOS: 69, 79 and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10730 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 27-bp 5'-untranslated region, a 1287-bp ORF, and a 1216-bp 3'-untranslated region. The ORF encodes a protein consisting of 428 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight of 48,992 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C19105) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10742> (SEQ ID NOS: 70, 80 and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10742 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 231-bp 5'-untranslated region, a 852-bp ORF, and a 828-

bp 3'-untranslated region. The ORF encodes a protein consisting of 283 amino acid residues and there existed two putative transmembrane domains. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was smaller than the molecular weight of 31,629 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35949) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03800> (SEQ ID NOS: 91, 101 and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03800 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 67-bp 5'-untranslated region, a 1431-bp ORF, and a 135-bp 3'-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed a

by the Kyte-Doolittle method, of the present protein. In



vitro translation resulted in formation of a translation product of 55 kDa that was almost identical with the molecular weight of 54,110 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Lys-Thr at position 81, Asn-Met-Thr at position 132, Asn-Val-Thr at position 307 and Asn-Gln-Thr at position 346). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mosquito vitellogenic carboxypeptidase (Accession No. P42660). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mosquito vitellogenic carboxypeptidase (VC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present

portion beginning from alanine at position 182 matched with



HP LTSDPSYFQNVGTGCSNYYNFLRC-TEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVE

\*... \*\*\*..\*\*\* \*.\*\*\*\*.. .\*. .... ..\*\*\* \*\*\*\*..\*\*\*\*. .\*.\*. .

VC LDGQESYFKKVTGFSSYYNFIKGDEESKQDSVLMEFLSNPEVRKGIHVGE LFPFHDSDGHN

5 HP K---YLREDTVQSVKPWLTEIMNNYKVLIYNGQLDIIVAAALTEHSLMGMDWKGSQEYKK

\* \*.\*\*\*..\* \*\*.....\*.\*\*.\* \*\*\*\* \* ..\* . \*\* \* ..\* . \*\*\*.

VC KVAEMLSEDTLDTVAPWVSKLLSHYRVLFYNGQLDIICAYPMTVDFLMKMPFDGDSEYKR

HP AEKKVWKIFKSDSEVAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDP

10 \*... \*.. \*.\*.\*\*\* ..\*\* ...\*.\*\*..\*\*..\* \*\*\* .\*\*\*\*\*.\*

VC ANRE---IYRVDGEIAGYKKRAGRLQEV LIRNAGHMVPRDQPKWAFDMITSFTHKNYL

HP YVG

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA095665) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

HP03831: (550 bp) Acc. No. U00000.1 (1990)

25

cDNA insert of clone HP03831 obtained from cDNA library of

human kidney revealed the structure consisting of a 191-bp 5'-untranslated region, a 681-bp ORF, and a 223-bp 3'-untranslated region. The ORF encodes a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human claudin-10 (Accession No. NP\_008915). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human claudin-10 (CD). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 76.2% in the entire region. The C-terminal region downstream from glycine at position 72 completely matched with that sequence.

HP MSRAQIWALVSGVGGFGALVAATTSNEWKVTTRASSVITATWVYQGLWMNCAGNALGS

..\* \*.. ..\* . . . . . \*\*\*.\* ...\*\*\*.. ...\*\*..\*.... \*

CD MASTASEIIAFMVSISGWVLVSSTLPTDYWKVSTIDGTVITTATYWANLWKACVTDSTGV

5 HP FHCRPHFTIFKVAGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

.\*. ... ..\*\*\*\*\*

CD SNCKDFPSMLALDGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

HP GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

10 \*\*\*\*\*

CD GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

HP FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

\*\*\*\*\*

15 CD FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

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Furthermore, the search of the GenBank using the  
base sequences of the present cDNA has revealed the  
20 registration of sequences that shared a homology of 90% or  
more (for example, Accession No. N41613) among ESTs. However,  
since they are partial sequences, it can not be judged

25

<HP03879> (SEQ ID NOS: 93, 103 and 113)

Determination of the whole base sequence of the cDNA insert of clone HP03879 obtained from cDNA library of human kidney revealed the structure consisting of a 33-bp 5'-untranslated region, a 918-bp ORF, and a 651-bp 3'-untranslated region. The ORF encodes a protein consisting of 305 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 34,073 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human NADH-cytochrome b5 reductase (Accession No. Y09501). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human NADH-cytochrome b5 reductase (CT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins showed a homology of 62.5%.

Table 23

---

HP MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRPQVTLLDPNEKYLLRLLDKTTVSHN

\* . \*\* \* . \*\* . \* . \*\* \*\*\*, \* . . . \*\*.

5 CT MGAQLSTLGHMVLFPVWFLYSLLMKLFQRS-TPAITLESPDIKYPLRLIDREIISHD

HP TKRFRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVVYKLG

\*, \*\*\*\*\*, . . \*, \*\*\*\*\*, \*\*\*\*\*, \*\*\*\*\*, \*\*, \*\*\*\*\*, . \*\*, \*, \*, \*\*\*\*\*, \*.

CT TRRFRFALPSPQHILGLPVGQHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVVYFKD

10

HP VHPKFPEGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKKSPPPEPRVAKKLG

. \*\*\*\*\*, \*\*\*\*\*, \* . . \*\*, . \*\*\*\*\*, \* \*\*\*\*, \*, \*, \*, \*\*\*\* \* \* . . \*, . \*

CT THPKFPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKKSNIIRTVKSVG

15

HP MIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLKW

\*\*\*\*\*, \*\*\*\*\*, \* \*, \*, \* \* \*\*\*\*\*, \*\* . \*\*\*\*, . . . . \*\*\*\*

CT MIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFLKW

HP FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQK

20

. \*\*\*, . \*, . \*, . \*, . \*\*, . . \*\*, \*\*, \*, . . . \*\*, \*\*\*\*\*, \* \*\* \*\*\*\*, . \*, . .

CT YTLDRAPEAWDYGQGFVNEEMIRDHLPPPEEPLVLMCGPPPMIYACLPNLDHVGHPTE

HP MDETH

25

CT RCFVF

---

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F06459) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10           <HP03880> (SEQ ID NOS: 94, 104 and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03880 obtained from cDNA library of human kidney revealed the structure consisting of a 98-bp 5'-untranslated region, a 684-bp ORF, and a 115-bp 3'-untranslated region. The ORF encodes a protein consisting of 227 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,717 predicted from the ORF. In this case, the addition

25   cleavage site of the secretory signal sequence, allows to



expect that the mature protein starts from aspartic acid at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat phosphatidylethanolamine-binding protein (Accession No. P31044). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat phosphatidylethanolamine-binding protein (RN). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the region of 133 amino acid residues other than the N-terminal region.

Table 24

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HP	MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV
20	
RN	MAADISQWAGPLSLQEVDPPQHALRVDYGGVTV
HP	VPDCAWPKLTQVWVWEEPCWPCATVLLGQDPAEDPNDGQWPKLKELEP
25	RN DELGKVLTPQVMNRPSSISWDGLDPGKLYTLVLTPDPAPSRKDPKFREWHHFLVNMKG

125

HP ADLKKGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKV---ISLLP-KENKTRGSWK

. \* . . \* . . . . . \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

RN NDISSGTV---LSEYVGSPPKDTGLHRYVWLVEEQEQLNCDEPILSNKSGDNRGKFK

5

HP MDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC

. . . \* . . . \* . . . \* . . . \* . . . \* . . . \* . . . \*

RN VESFRKKYHLGAPVAGTCFQAEWDDSVPKLHDQLAGK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H83784) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15

<HP10704> (SEQ ID NOS: 95, 105 and 115)

20

Determination of the whole base sequence of the cDNA insert of clone HP10704 obtained from cDNA library of human kidney revealed the structure consisting of a 141-bp 5'-untranslated region, a 1326-bp ORF, and a 399-bp 3'-untranslated region. The ORF encodes a protein consisting of

25

transmembrane domains. Figure 35 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5                   The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human unknown gene product (Accession No. AAC27544). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention  
10                   (HP) and human unknown gene product (UP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins  
15                   shared a homology of 39.1% in the entire region.

Table 25

---

HP	MATHKALVMCI.GLPLFLPG-AWAQGHVPPGCSQGLNPLYYNLCDRSGAWGIVLE
20	* **.... * ... **.. * * * .*** .. ****.*
UN	MFVASERKMRAHQVLTFLLLFVITSVASENASTSRGCGLDLLPQYVSLCDLDAIWGIVVE
UP	AVAGAGITLTLMLILLVRLPFIKEKEKSPVGLHFLFLGLTGLFGLTFAFIQDEET
25	UN AVAGAGALITLLMLILLVRLPFIKEKEKSPVGLHFLFLGLTGLFGLTFAFIQDEET

127

HP TCASRRFLFGVLFALCFSCLAHVFAFNFLARKNHGPRGWVIFTVALLLTLVEVIINTEW

. \*. \*\*\*\*.\*\*\*\*\*.\*\*\*\*\* ..... \*.\*. \*\* \*\* . . \*\* \* \*\*.\*\*\*.\*\*\*

UN ICSVRRFLWGVLFAFCFSCLLSQAWRVRLVRHGTGPAGWQLVGLALCLMLVQVIIAVEW

5

HP LIITLVRGSGEGGPQGNSSAGWAVASPCAIANMDFVMALIYVMLLLLGAFLGAWPALCGR

\*.\*.\*. \* .. ..\*\* . \*\*\*\*\* \*.\*\*.. \* .\*\*\*.

UN LVLTVLR-----DT-----RPACAYEPMDFVMALIYDMVLLVVTGLALFTLCGK

10

HP YKRWRKHGVFVLLTTATSVAIWVWVIMYTYGN-KQHNSPTWDDPTLAIALAANAWAFVL

.\*\*\*. \*.\*\*.\*.\*. \*\* \*\*.\*.\*.\*\*\* \* ... \*.\*\*\*\*\*.\*\*\*.\*.\*.\*.

UN FKRWKLNGAFLITAFSLVLIWVAWMTMYLFGNVKLQQGDAWNDPTLAITLAASGWVFVI

HP FYVIPEVSQVTKSSPEQSYQGDMYPTRGVGY-ETILKEQ-KGQSMFVENKAFSMDEPVAA

15

\*.\*.\*. \* .. \*. . . \*. \*\* ..\* . . . .\*\*\*\*\*. \*\*

UN FHAIPEI-HCTLLPALQENTPNYFDTSQPRMRETAFEEDVQLPRAYMENKAFSMDEHNAA

HP KRPVS-PYSGYNGQLLTSVYQPTMALMIKVPSEGAYDIILPRATANSQVMGSANSTLRA

\*... \* .. . \*. .... . \* .. . \* . \* .. . . \*.

20

UN LRTAGFPNGSLGKRPSGSLGKRPSAPFRSNVYQPTEMAVVLNGGTIPTAPPSTGRHLW

HP EDMYSAQSHQAATPPKDGKNSQVFRNPYVWD

25

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA346702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
5 encode the same protein as the protein of the present invention.

<HP10715> (SEQ ID NOS: 96, 106 and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10715 obtained from cDNA library of  
10 human umbilical cord blood revealed the structure consisting of a 49-bp 5'-untranslated region, a 798-bp ORF, and a 1351-bp 3'-untranslated region. The ORF encodes a protein consisting of 265 amino acid residues and there existed two putative transmembrane domains. Figure 36 depicts the  
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was larger than the molecular weight of 29,217 predicted from the ORF.

20 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA346702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
25 encode the same protein as the protein of the present

invention.

<HP10724> (SEQ ID NOS: 97, 107 and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10724 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 68-bp 5'-untranslated region, a 627-bp ORF, and a 1485-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was almost identical with the molecular weight of 23,850 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T78035) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10733> (SEQ ID NOS: 98, 108 and 118)

human umbilical cord blood revealed the structure consisting

of a 102-bp 5'-untranslated region, a 1203-bp ORF, and a 222-bp 3'-untranslated region. The ORF encodes a protein consisting of 400 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was larger than the molecular weight of 43,151 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 52, Asn-Ala-Ser at position 131, Asn-Ile-Thr at position 145 and Asn-Leu-Ser at position 343). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 33.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH (Accession No. P06002) and *Drosophila melanogaster* of the present invention (HP) and *Drosophila melanogaster*

GOLIATH protein (DM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the entire region.

Table 26

---

10	HP MAWRRREASVGARGVLALALLALALCVPGARGRALEWFSAVVNIEYVDPQTNLTVWSVSE
	HP SGRFGDSSPKEGAHGLVGVPWAPGGDLEGCAPDTRFFVPEPGGRGAAPWVALVARGGCTF
	HP KDKVLVAARRNASAVVLYNEERYGNITLPM SHAGTGNIVVIMISYPKGREILEL-VQKGI
15	* *... ..*.*. . *.*...*
	DM MQLKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGY
	HP PVTMTIGVGTRHVQEF--ISGQSVVFVAIAFITMMIISLAWLIFYIQRFLY-TGSQIGS
	**..* * * *... .. **, **, *, ** . * ***** * ... *
20	DM NVTISIIEGRRGVRTISSLNRTSVLFVSISFI--VDDILCWLIFYIQRFRYMQAKDQQS
	HP QSHRKETKKVIGQLLLHTVKHGEKGIDVDAENCAVCIENFKVKDIIRILPCKHIFHRICI
	*** * * * * * * * * * * * * * * *



HP DPWLLDHRTCPMCKLDVIKALGYWGE PGDVQEMPAPESPPGRDPAANLSLALPDDGGSDE

\*\*\*\*.\*\*\*\*\*.\* \*\* ... .\*. \* .. .. .

DM DPWLIEHRTCPMCKLDVLKFGY-VVGDQIYQTPSPQHTAPIASIEEVPVIVVAVPHGPQ

5 HP SSPPSASPAESEPCDPSFKGDAGENTALLEAGRSDSRHGGPIS

. . \* . . . \* . . . \* . . . . .

DM PLQPLQASNMSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRRNSAPATMP

10           The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. AI286184) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
15 encode the same protein as the protein of the present  
invention.

<HP10734> (SEQ ID NOS: 99, 109 and 119)

Determination of the whole base sequence of the  
cDNA insert of clone HP10734 obtained from cDNA library of  
20 human umbilical cord blood revealed the structure consisting  
of a 124-bp 5'-untranslated region, a 579-bp ORF, and a  
1202-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 192 amino acid residues and there existed one  
25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human sodium channel  $\beta 2$  subunit (Accession No. AAD47196). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human sodium channel  $\beta 2$  subunit (SC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 26.3% in the N-terminal region of 152 amino acid residues.

Table 27

---

HP	MFCPLKLILLPVLLDYSGLNDLNVS-PPELTVHVGDSALMGCVFQS--TEDK
20	...*. *..... ....*. *.*.* *.*. *.*.* *..
	SC MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTPATLNVLNQSDARLPCTFNSCYTVNH
25	SC KQFSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMILRNVPQE

HP DQGTIYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVTKVE

\*,\*,\* \* \*. ... . \*.\*\* \*\*\* \* \*. ..

SC DEGIYNCYIMNPPDRHRGHGKIHLQVLMEEPPERDFTVAVIVGASVGGFLAVVILVLMVV

5

HP WIFSGRRRAKVTRRKHHCVREGSG

SC KCVRRKKEQKLSTDDLKTEEEGKTDGEGNPDDGAK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C03216) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10756> (SEQ ID NOS: 100, 110 and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10756 obtained from cDNA library of human kidney revealed the structure consisting of a 49-bp 5'-untranslated region, a 783-bp ORF, and a 166-bp 3'-

secretory signal at the N-terminus. Figure 40 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,356 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW027769) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03670> (SEQ ID NOS: 121, 131 and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03670 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 77-bp 5'-untranslated region, a 1014-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 337 amino acid residues and there existed at least seven putative transmembrane domains. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid

protein was similar to human hypothetical protein KIAA0260

(Accession No. BAA13390). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0260 (KI). Therein, the marks of -, \*, and . represent

5 a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.6% in the entire region other than the N-terminal region. In

10 addition, the C-terminal region beginning from leucine at position 77 matched with human putative Sqv-7-like protein (Accession No. AJ005866) except one amino acid residue.

Table 28

15

HP

MTAGGQAEAEGAGGEPG

KI NSWSPLGAAAAGPRAARPRRQATAAAAAAMAEVHRRQHARVKGEAPAKSSTLRDEEELGMA

20

HP AARLPSRVARLLSALFYGTCSFLIVLVNKAALLTTYGFPSPIFLGIGQMAATIMILYVSKL

. \*\*. \* \*\*\*. . \*\*\*\*\*. \*\*\*. \*\*. \* \*\*\*. . . \*. \*\*\*. \*\*. . \*. \*. \*

KI SAETLTVFLKLLAAGFYGVSSFLIVVVNKSFLTNYRFPSSLCVGLGQMVA TVAVLWVGKA

25

.... \*\*\*. \*. . . \* \* \*\*\*\*\* \*\*\*. \*. \*\* \*\*\*. \*\*. \*\*\*\*\*. \*. \* . \*. . \*. .

KI LRVVKFPDLDRNVPRKTFPLPLLYFGNQITGLFSTKKLNLPMTVLRRFSILFTMFAEGV

HP ILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLNDIFTAANGVYTKQKMDPK

. \* \* . \* . \* . . \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \*

5 KI LLKKTFSWGIKMTVFAMIIGAFVAASSDLAFDLEGYAFILINDVLTAANGAYVKQKLDISK

HP ELGKYGVLFYNACFMIIPTLIISVSTGDLQQATEFNQWKNNVFILQFLLSCFLGFLLMYS

\* \* \* \* \* . \* . \* \* \* \* \* . \* \* \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \*

KI ELGKYGLLYNALFMILPTLAIAYFTGDAQKAVEFEGWADTLFLLQFTLSCVMGFILMYA

10

HP TVLCSYYNSALTTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRYSFRTL

\* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \*

KI TVLCTQYNSALTTTIVGCIKNILITYIGMVFGGDYIFTWTNFIGLNISIAGSLVYSYITF

15 HP SSQLKPKPVGEENICLDLKS

. . . . \* . \* . \* \* \* . \*

KI TEEQLSKQ-SEANNKLDIKGKGAV

20

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R24922) among ESTs. However, since they are

25

encode the same protein as the protein of the present

invention.

<HP03688> (SEQ ID NOS: 122, 132 and 142)

Determination of the whole base sequence of the cDNA insert of clone HP03688 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 35-bp 5'-untranslated region, a 711-bp ORF, and a 1729-bp 3'-untranslated region. The ORF encodes a protein consisting of 236 amino acid residues and there existed five putative transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein W02D9 (Accession No. CAB03470). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein W02D9 (CE). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The similarity of the amino acid sequence of the present invention to that of the protein of the present invention is 50.8% in the entire region other than the N-terminal

region.

Table 29

---

5	HP	MAEAEE
	CE	MEILNLSSKFSLSDKPCQKFIFSLFSAVQNSRFKIISFPEIHQKPLPQEEMNSFGNASVD
	HP	SPGDPGTASPRPLFAGLSDISISQDIPVEGEITIPMRSRIREFDSSTLNESVRNTIMRDL
10		**.. . . **. *. *. *. **.
	CE	IDMLEQEMAAEQTANLSGNIAGMSAPKSSSNRRGPMQEVDLDAEFDTLLEPVWDTVKRDV
	HP	KAVGKKFMHVLYPR-KSNTLLRDWDLWGPLILCVTLALMLQRDSADSEKDGGPQFAEVFV
		. ** ** *. *. . . . *****. **. ***. **. . . . . ***. **.
15	CE	LTVGAKFTHVVLPHGDKQQLLRDWDWGPLFICVGLALLLQH---NGGTESAPQFTQVFT
	HP	IVWFGAVTITLNSKLLGGNISFFQSLCVLGYCILPLTVAMLICRLVLLADPGPVNFMVRL
		*. **. *. *. * *****. ***. ** ** .. *. *. *. . . *. **
	CE	ITFFGSVIVTANIKLLGGNISFFQSLCVIGYCLIPPFVAAVLCSL-FLHGI---AFPLRL
20	HP	FVVIVMFAWSIVASTAFLADSQPPNRRALAVYPVFLFYFVISWMILTFTPQ
		... . *. **. ** . ***. **. . . * *. *****. ****. .
		.....
25		



Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T51465) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03825> (SEQ ID NOS: 123, 133 and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03825 obtained from cDNA library of human kidney revealed the structure consisting of a 20-bp 5'-untranslated region, a 1683-bp ORF, and a 36-bp 3'-untranslated region. The ORF encodes a protein consisting of 560 amino acid residues and there existed seven putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was smaller than the molecular weight of 64,047 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the

Table 30 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and Mycobacterium tuberculosis hypothetical protein Rv0235c (MT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the entire region other than the N-terminal region. In addition, the region from alanine at position 293 to proline at position 502 matched with human putative novel protein c360B4.1 (Accession No. CAB56180).

Table 30

---

15	HP MAAPAESLRRRKTGYSDPEPESPPAPGRGPAGSPAHLHTGTFWLTRIVLLKALAFVYFVA	
		. . . . *. *. *. * . . *. *. *. *
	MT	MGWFSAPPEYWLGRALALERGTATIIYLIA
	HP FLVAFHQNKQLIGDRGLLPCRVLKKNFQQYFQDRTSWEVFSYMPITLWLMDSMNSNLD	
20	*. *. *. * . . *. *. *. *. *. * . . *. * . . . * . . . *	
	MT FVAAAQQFRPLIGEHGMLPVPRYLAG-QSFWRTPSIFH-FRYSDRVFAVCW--LGAVLS	
	HP LLALLGLGISSFVLITGCANMLLMAALWGLYMSLVNVGHVWY/SFGWESQLLETGFLGIFL	
	MT AAVVAGAAASFVFLR ATMLIWLTLWVLIYLSIVNVQAWYSFGWESULLLETGFLMIFL	



HP SLEELRPYFRDRGWPLPGPL

\*\* ..

MT SLRKVASPPAD

---

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA019047) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03877> (SEQ ID NOS: 124, 134 and 144)

15 Determination of the whole base sequence of the cDNA insert of clone HP03877 obtained from cDNA library of human kidney revealed the structure consisting of a 106-bp 5'-untranslated region, a 1221-bp ORF, and a 678-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed four putative transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro

20

25 of 46,208 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein Y37D8A (Accession No. CAA21543). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein Y37D8A (CE). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.2% in the intermediate region of 329 amino acid residues.

Table 31

---

HP	MAENG
CE	MAKKQKKSTEKSERTVEFKEPPK PANSEERLVSTRQFLAKIGQKKLIK KVKNF RF SKKT
HP	KNCDQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNI VLWRQPLITLQYFSLEILVIL
	. * ** . ** . ** . * * . . * . * .
CE	FIDFFSENQKKNCRLKPAGRGMKPSQSNTLNRMERETIVFWRRPHIVIPYALMEIAHLA
HP	KWISKLWIRQSIVVSFLILLAVLTATYVGVHQYVQRTEKQFLIYAWIGLGLISG



of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T18977) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
5 encode the same protein as the protein of the present invention.

<HP10765> (SEQ ID NOS: 125, 135 and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10765 obtained from cDNA library of  
10 human umbilical cord blood revealed the structure consisting of a 30-bp 5'-untranslated region, a 1362-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 453 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative  
15 transmembrane domain in the inner portion. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was almost identical with the molecular  
20 weight of 47,724 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of  
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10766> (SEQ ID NOS: 126, 136 and 146)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP10766 obtained from cDNA library of  
human kidney revealed the structure consisting of a 150-bp  
5'-untranslated region, a 180-bp ORF, and a 675-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
59 amino acid residues and there existed two putative  
10 transmembrane domains. Figure 46 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 10 kDa or less that was almost identical with the  
15 molecular weight of 6,098 predicted from the ORF.

The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. T85491) among ESTs. However, since they are  
20 partial sequences, it can not be judged whether or not they  
encode the same protein as the protein of the present  
invention.

25 cDNA insert of clone HP10770 obtained from cDNA library of



human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 633-bp ORF, and a 186-bp 3'-untranslated region. The ORF encodes a protein consisting of 210 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was larger than the molecular weight of 22,156 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792771) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10772> (SEQ ID NOS: 128, 138 and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10772 obtained from cDNA library of human kidney revealed the structure consisting of a 19-bp 5'-untranslated region, a 498-bp ORF, and a 724-bp 3'-

transmembrane domains. Figure 48 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5           The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11871) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
10       encode the same protein as the protein of the present invention.

<HP10773> (SEQ ID NOS: 129, 139 and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10773 obtained from cDNA library of  
15       human kidney revealed the structure consisting of a 186-bp 5'-untranslated region, a 489-bp ORF, and a 499-bp 3'-untranslated region. The ORF encodes a protein consisting of 162 amino acid residues and there existed four putative transmembrane domains. Figure 49 depicts the  
20       hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

25       of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. N33828) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10776> (SEQ ID NOS: 130, 140 and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10776 obtained from cDNA library of human kidney revealed the structure consisting of a 207-bp 5'-untranslated region, a 666-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 221 amino acid residues and there existed three putative transmembrane domains. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 24,883 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI929639) among ESTs.

protein of the present invention.

## INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized

25

The present invention also provides genes

corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include  
5 contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements.  
10 The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate  
15 genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified  
20 expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through

25 Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254;

Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein).

Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided.

Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms

are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s).

Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA

reference herein), or through homologous recombination,

preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are  
5 incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development  
10 of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such  
15 forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known  
20 techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present

25 most preferably at least 75%) of the length of a disclosed

protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a

the disclosed polynucleotides or proteins; that is,



naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

5           The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

          The present invention also includes polynucleotides capable of hybridizing under reduced  
10           stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for  
15           example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp) <sup>1</sup>	Hybridization Temperature and Buffer <sup>1</sup>	Wash Temperature and Buffer <sup>1</sup>
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T <sub>B</sub> *; 1×SSC	T <sub>B</sub> *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T <sub>D</sub> *; 1×SSC	T <sub>D</sub> *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T <sub>F</sub> *; 1×SSC	T <sub>F</sub> *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T <sub>H</sub> *; 4×SSC	T <sub>H</sub> *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T <sub>J</sub> *; 4×SSC	T <sub>J</sub> *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T <sub>L</sub> *; 2×SSC	T <sub>L</sub> *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T <sub>N</sub> *; 6×SSC	T <sub>N</sub> *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T <sub>P</sub> *; 6×SSC	T <sub>P</sub> *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T <sub>R</sub> *; 4×SSC	T <sub>R</sub> *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub> : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C)=81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41 (%G+C) - (600/N), where N is the

1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

## CLAIMS

1. A protein comprising any one of an amino acid  
sequence selected from the group consisting of SEQ ID NOS: 1  
5 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2. An isolated DNA encoding the protein according to  
Claim 1.

3. An isolated cDNA comprising any one of a base  
sequence selected from the group consisting of SEQ ID NOS:  
10 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4. The cDNA according to Claim 3 consisting of any  
one of a base sequence selected from the group consisting of  
SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141  
to 150.

15 5. An expression vector that is capable of expressing  
the DNA according to any one of Claim 2 to Claim 4 by in  
vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of  
expressing the DNA according to any one of Claim 2 to Claim  
20 4 and of producing the protein according to Claim 1.

7. An antibody directed to the protein according to  
Claim 1.

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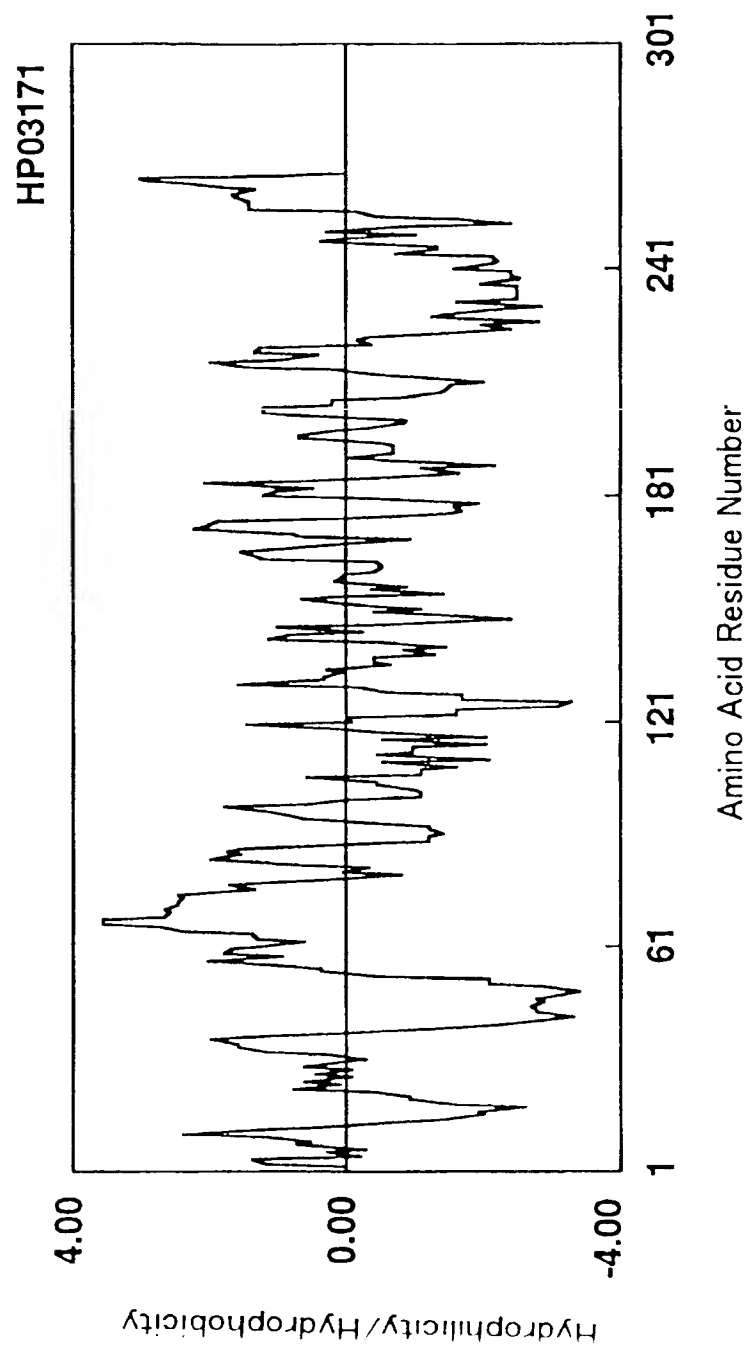


Fig.1

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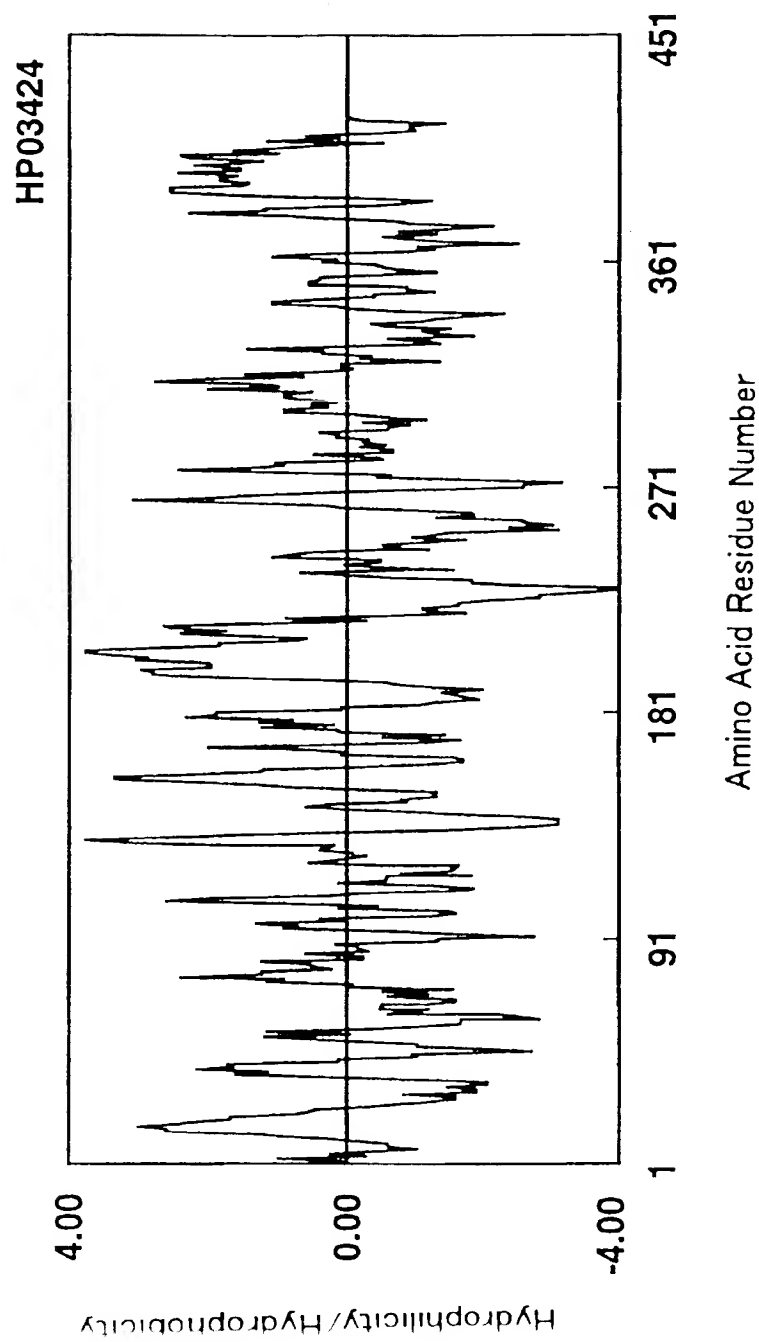


Fig.2

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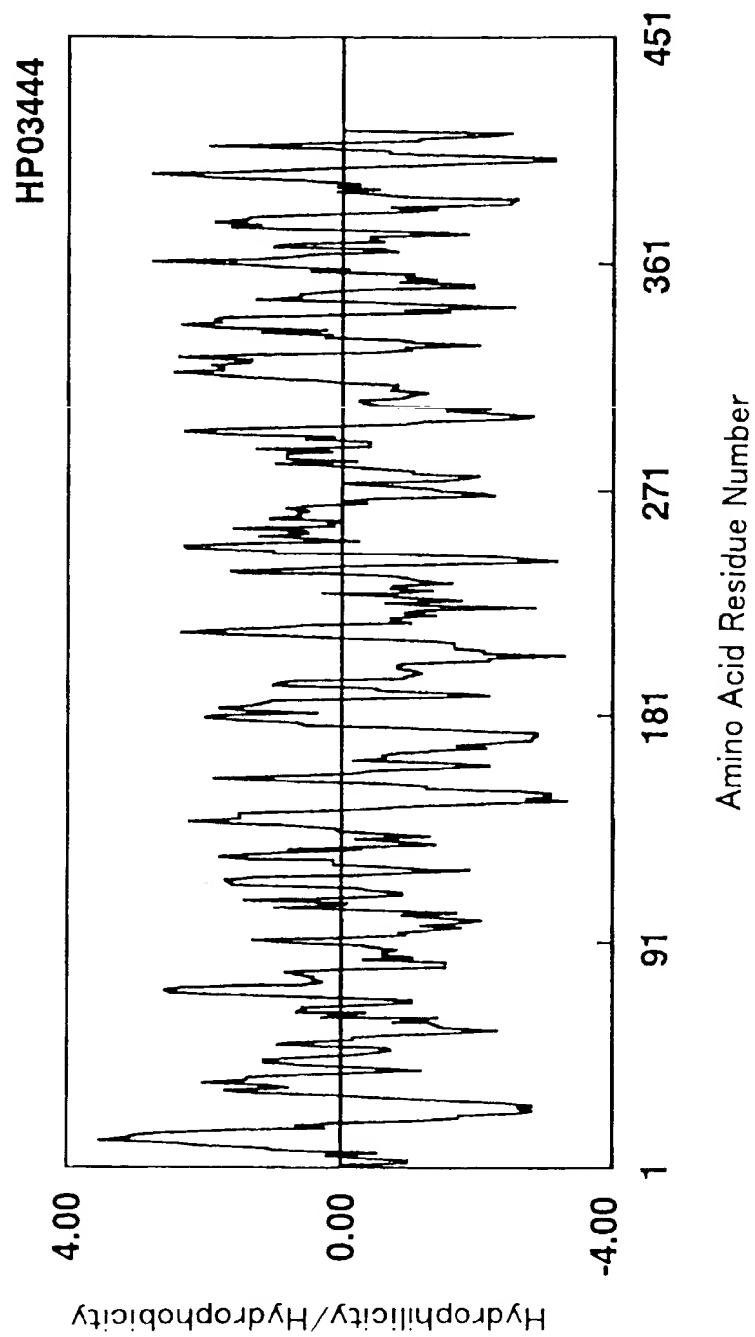


Fig.3



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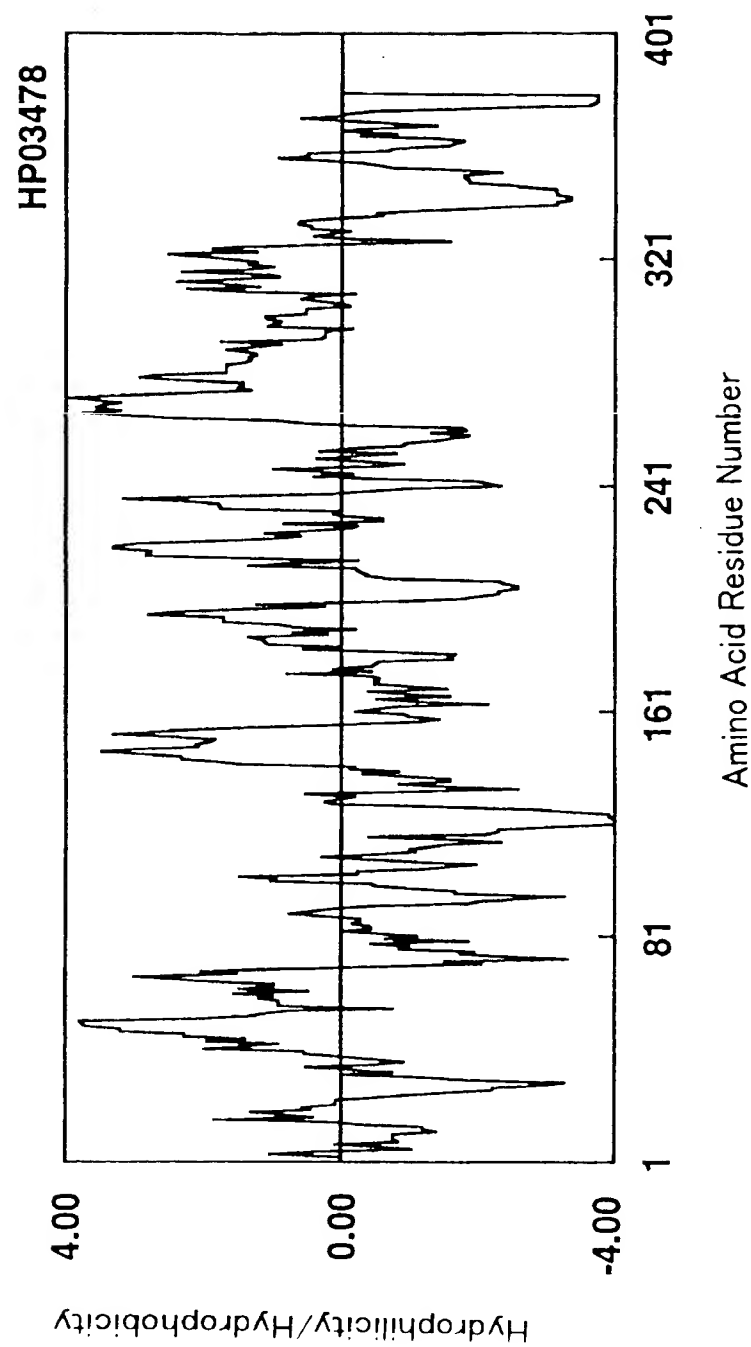


Fig.4

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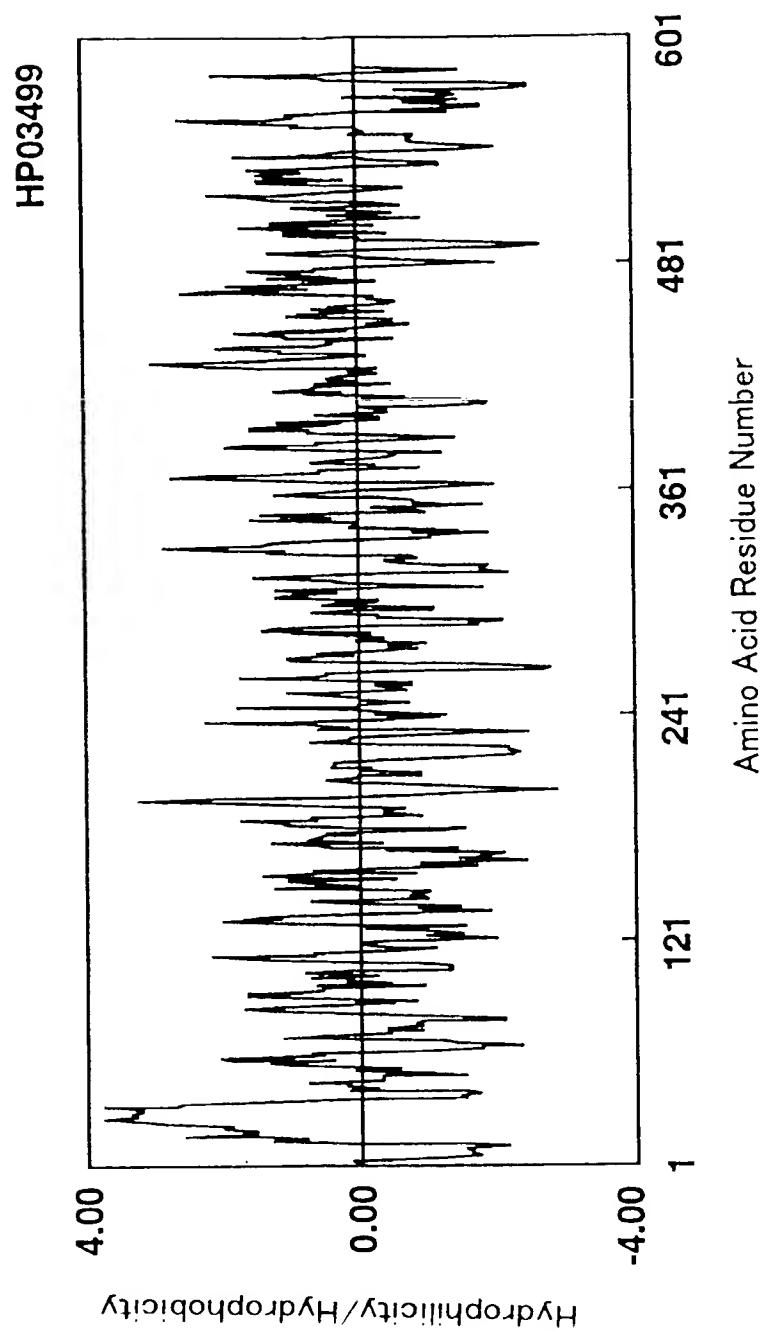


Fig.5

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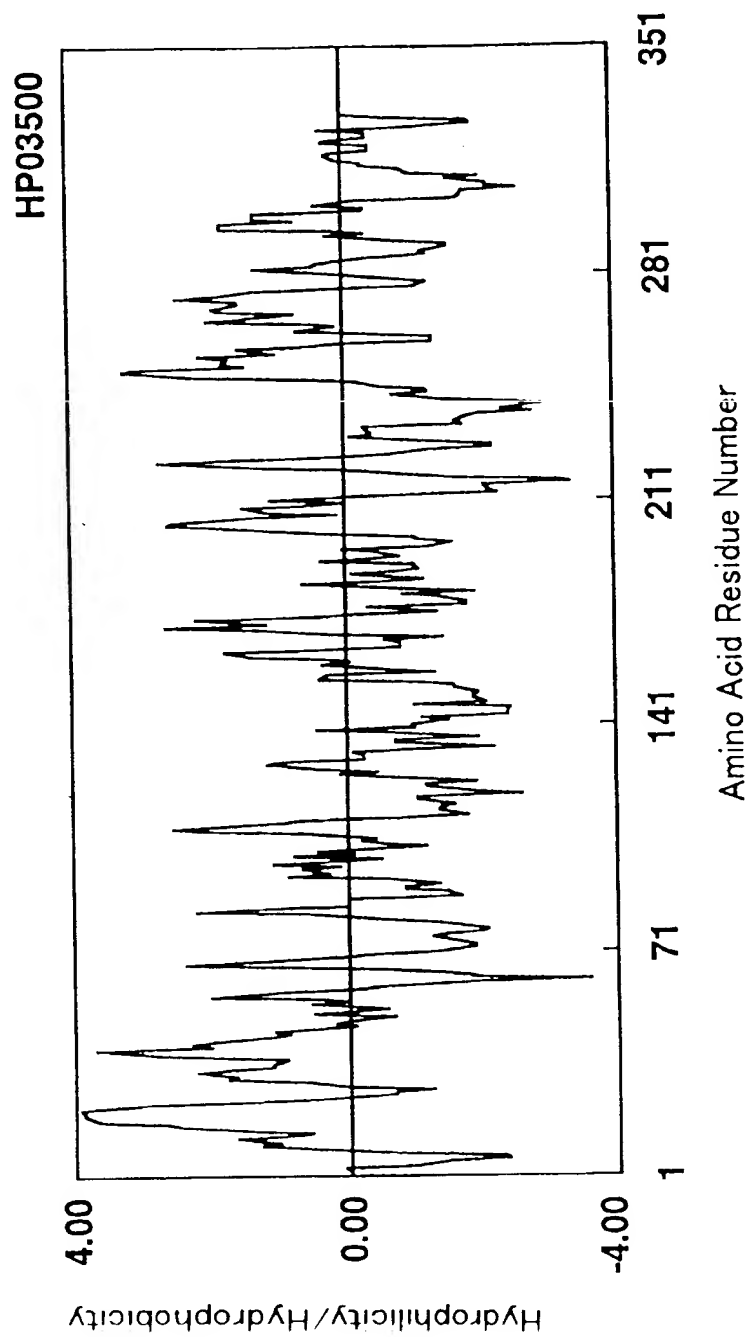


Fig.6

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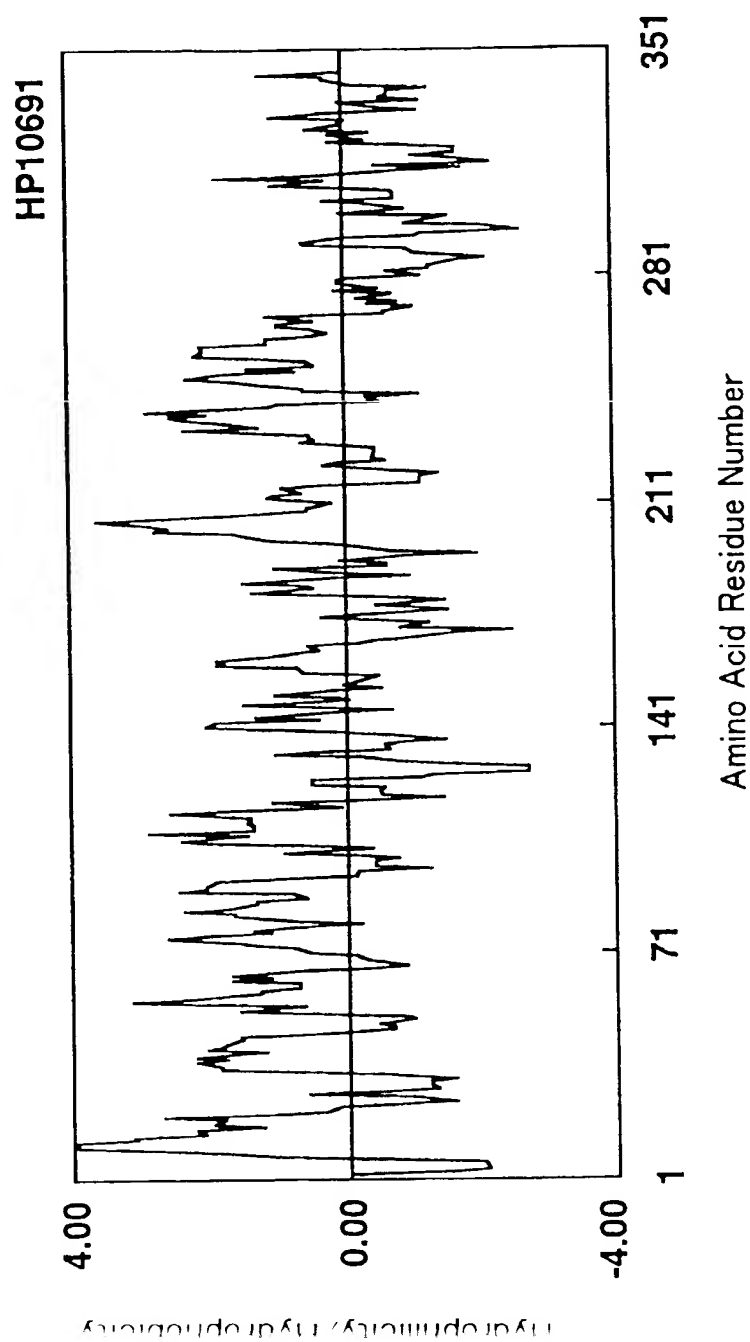


Fig.7

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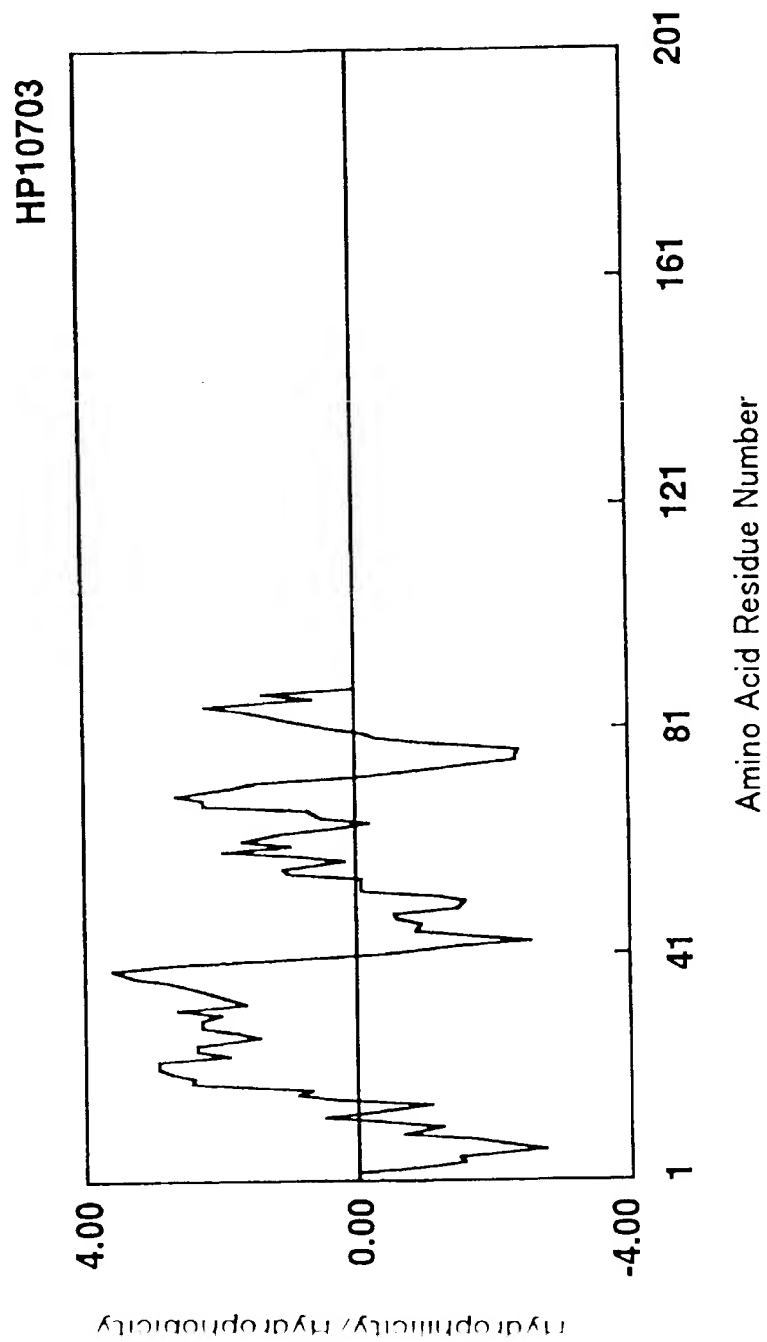


Fig.8

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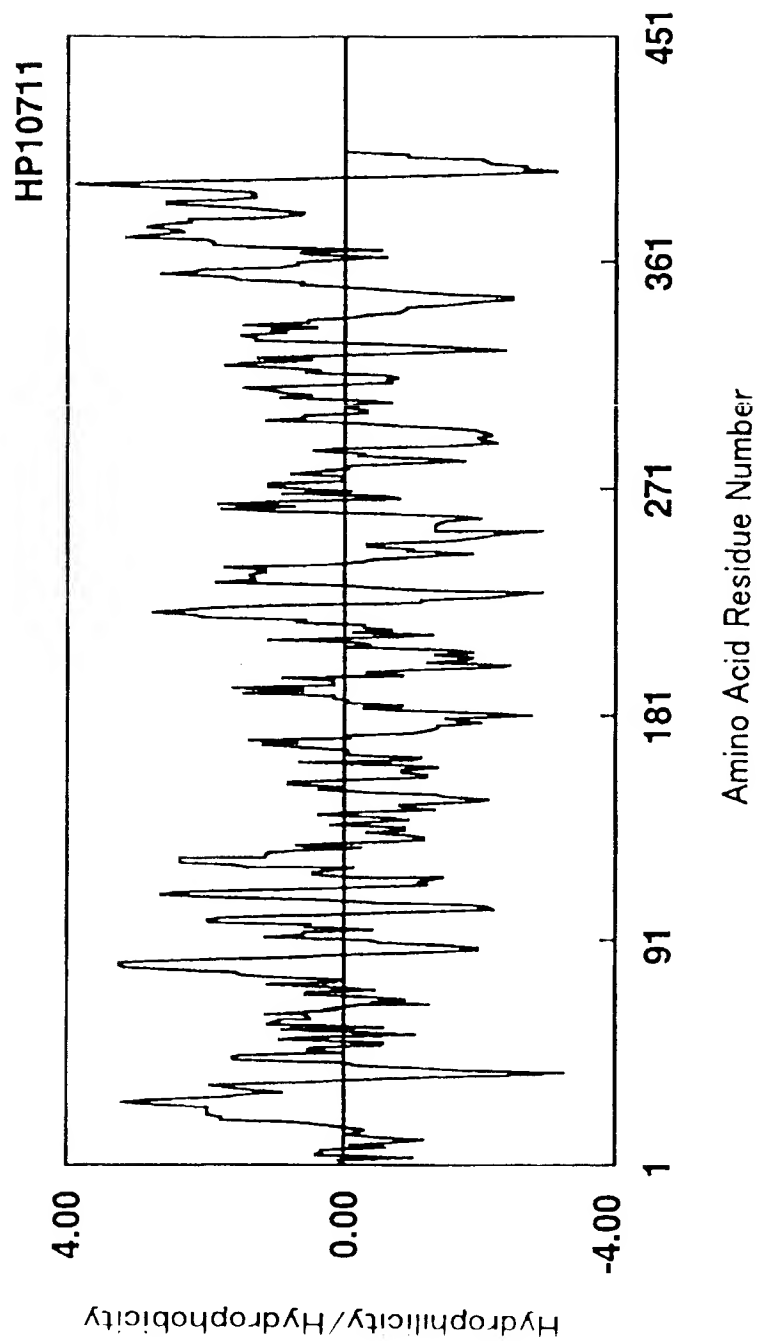


Fig.9

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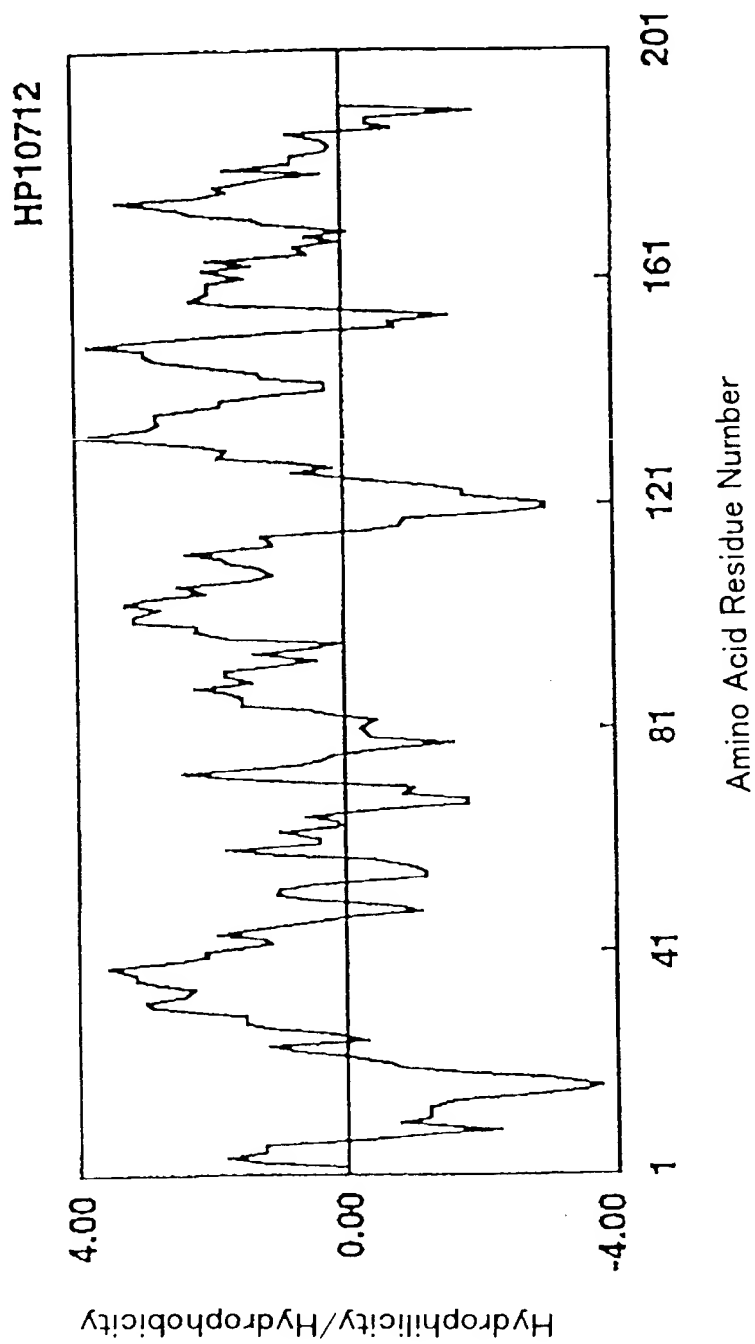


Fig.10

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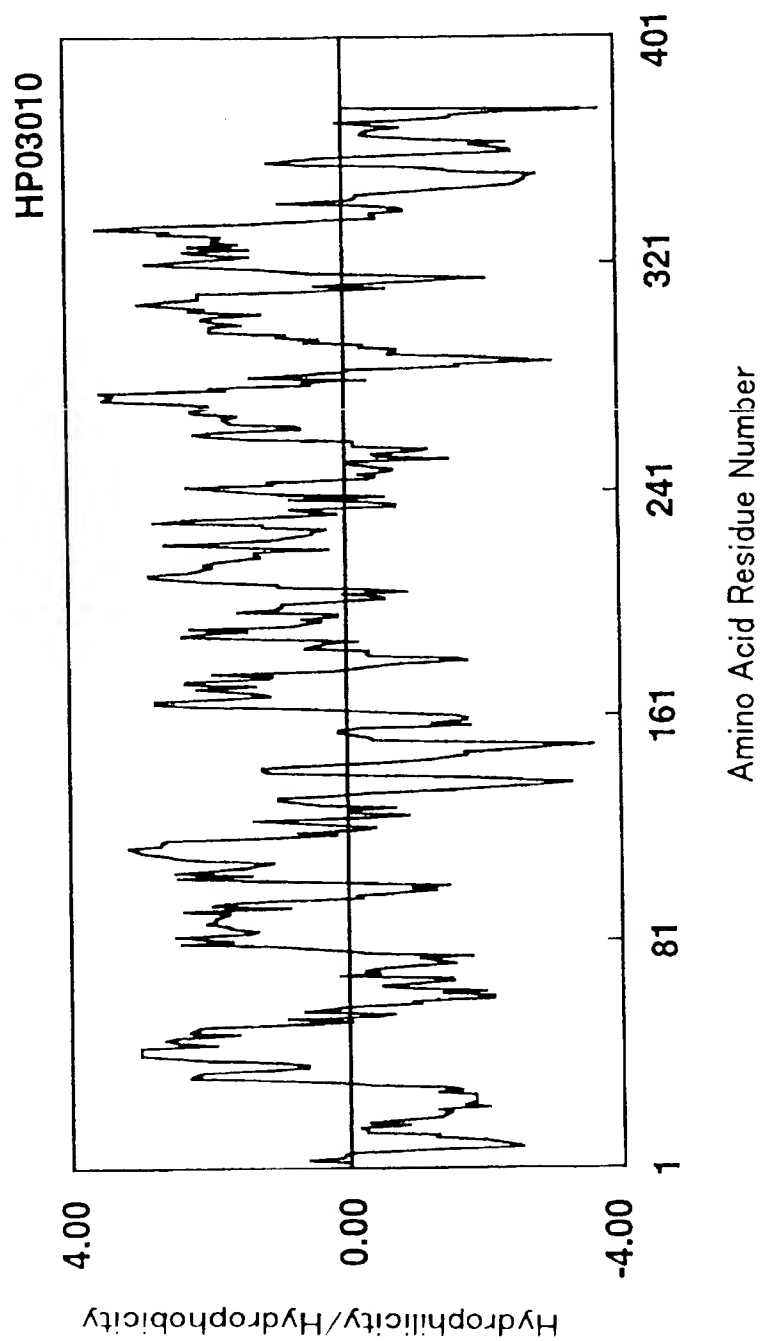


Fig.11



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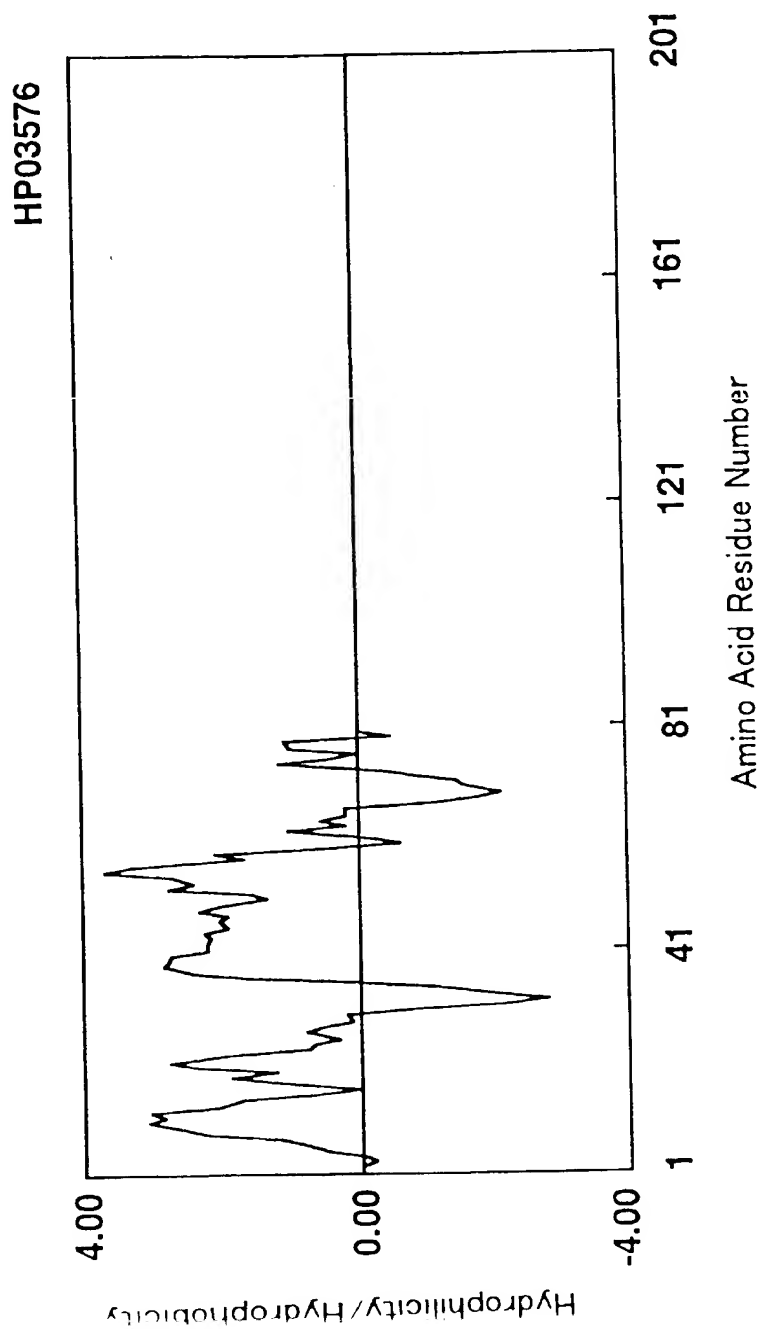


Fig.12

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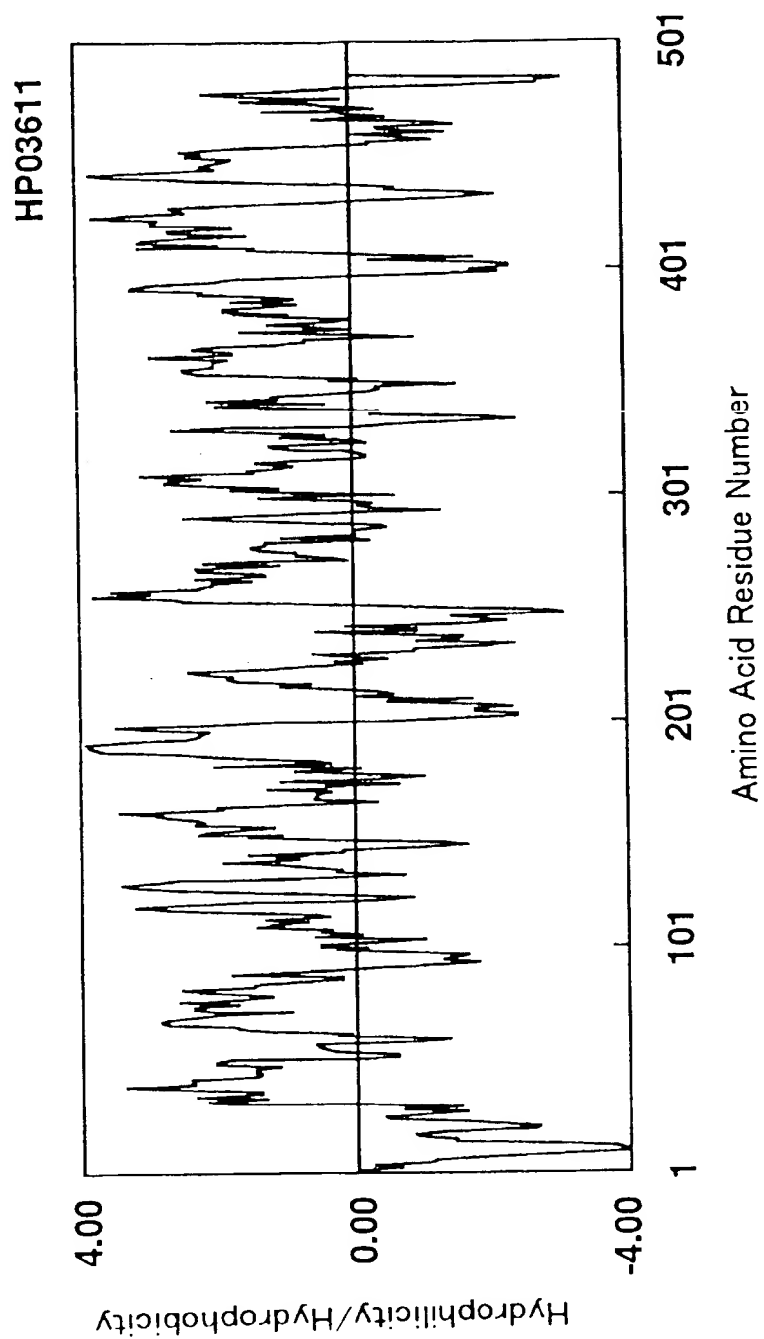


Fig.13

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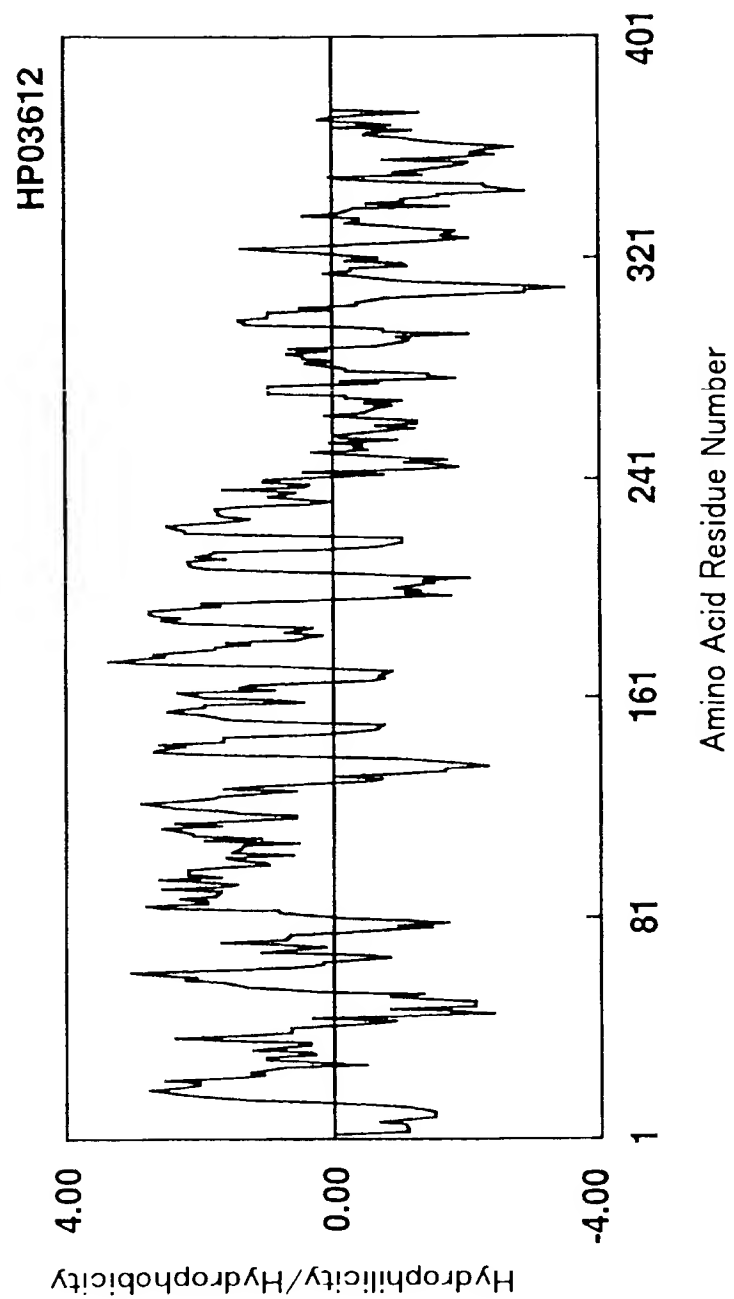


Fig. 14

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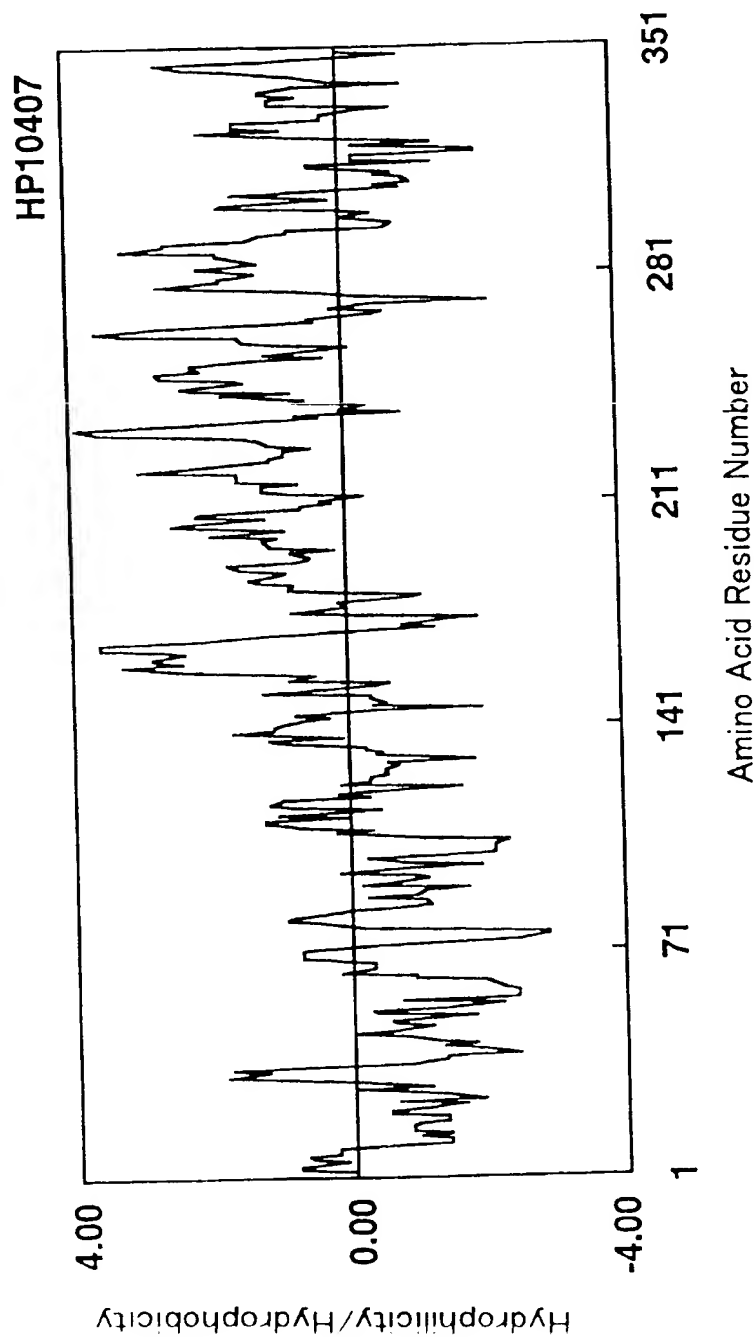


Fig.15

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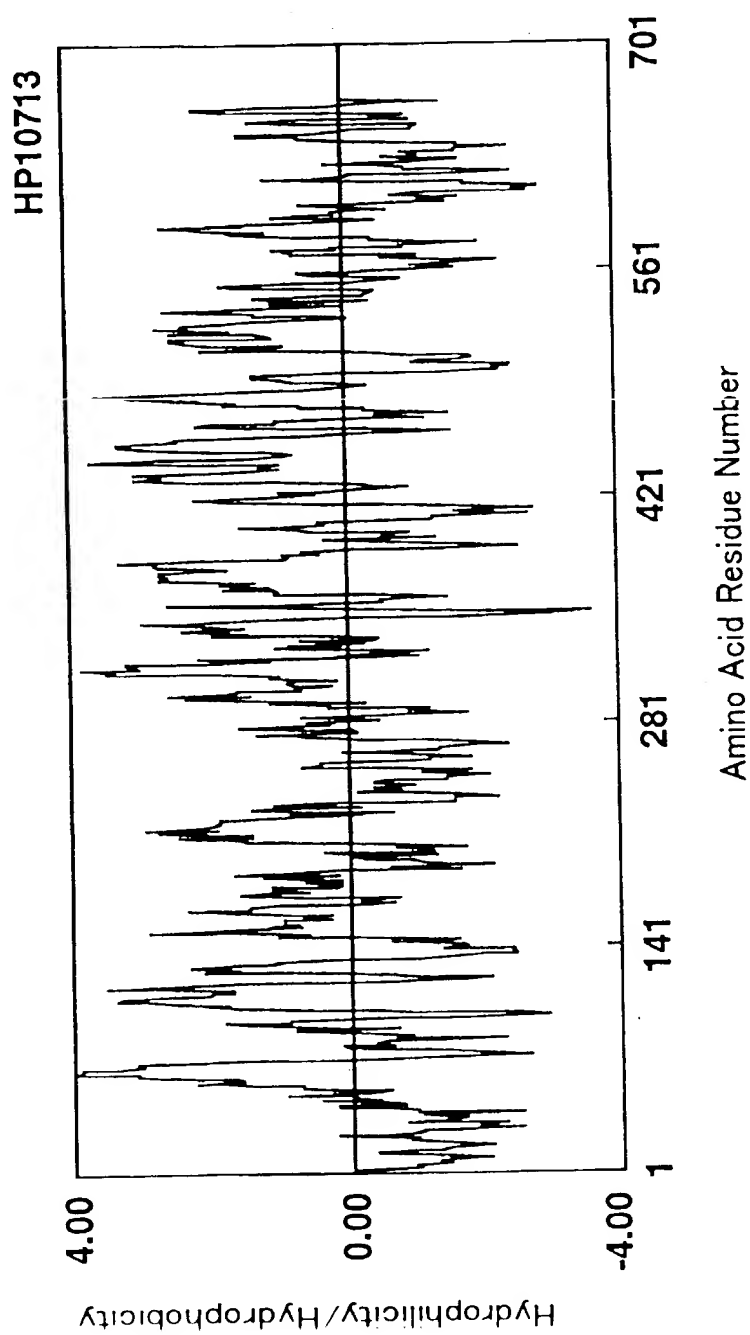


Fig.16

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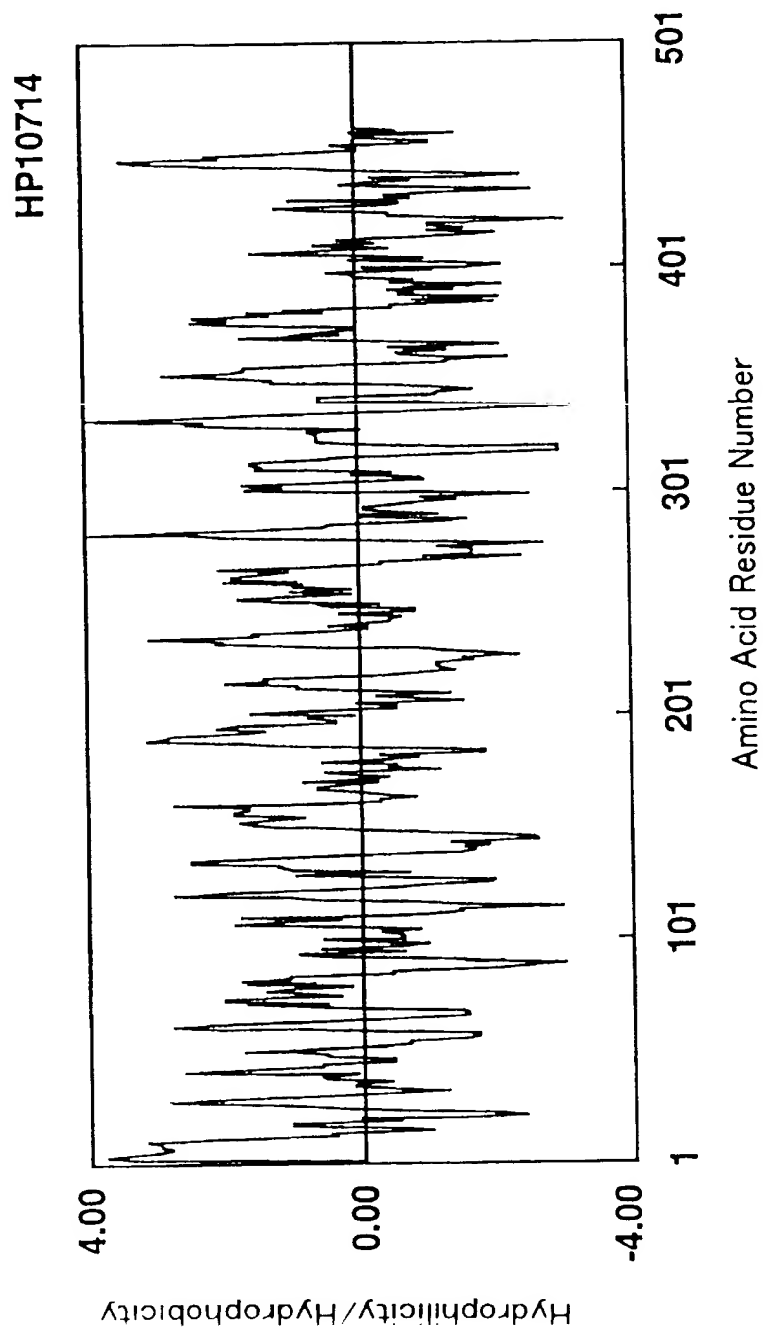


Fig.17

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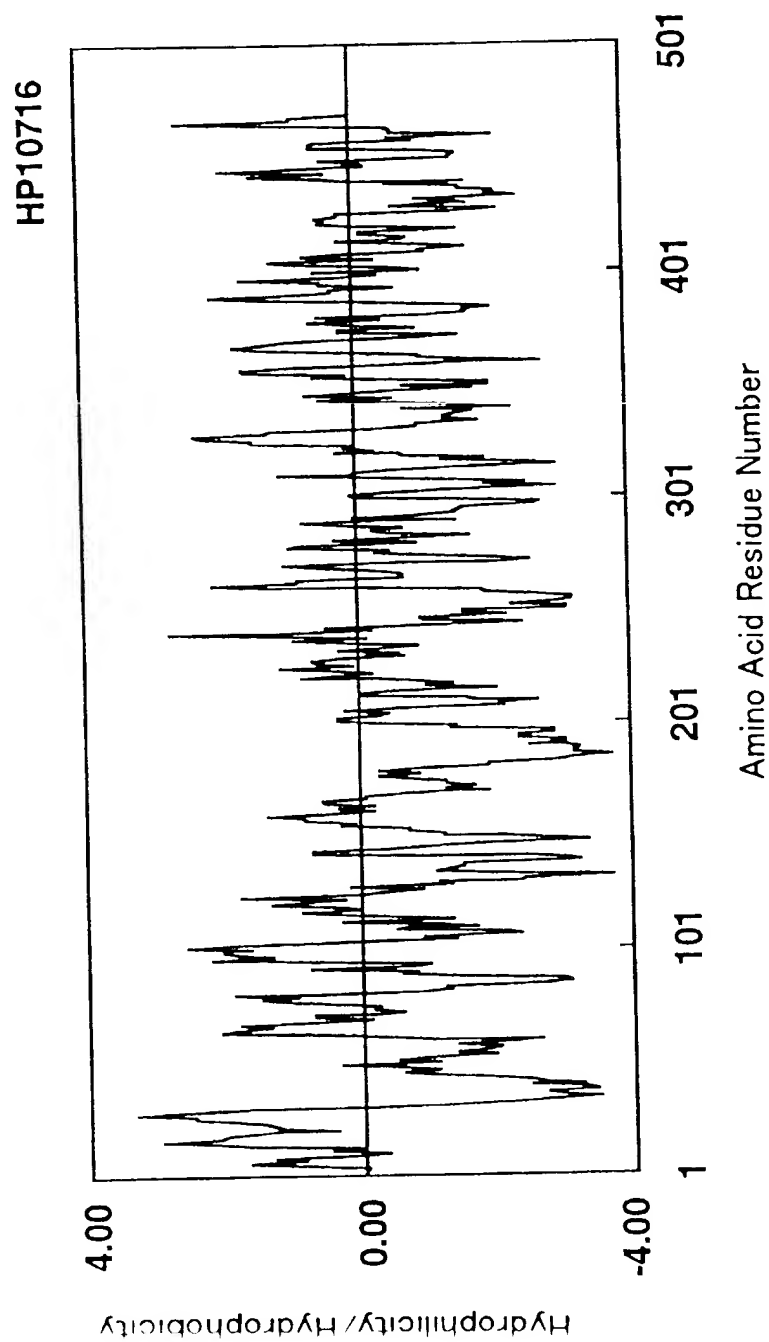


Fig.18

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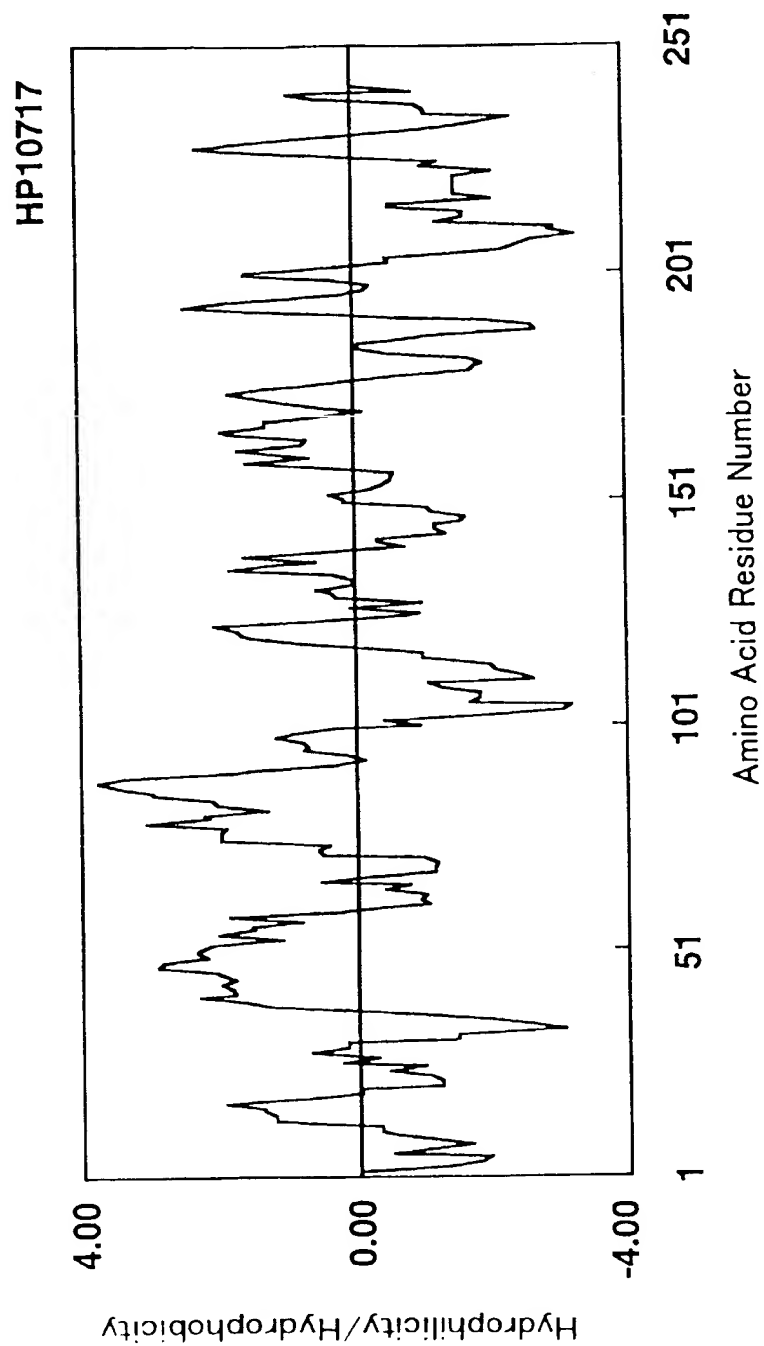


Fig.19



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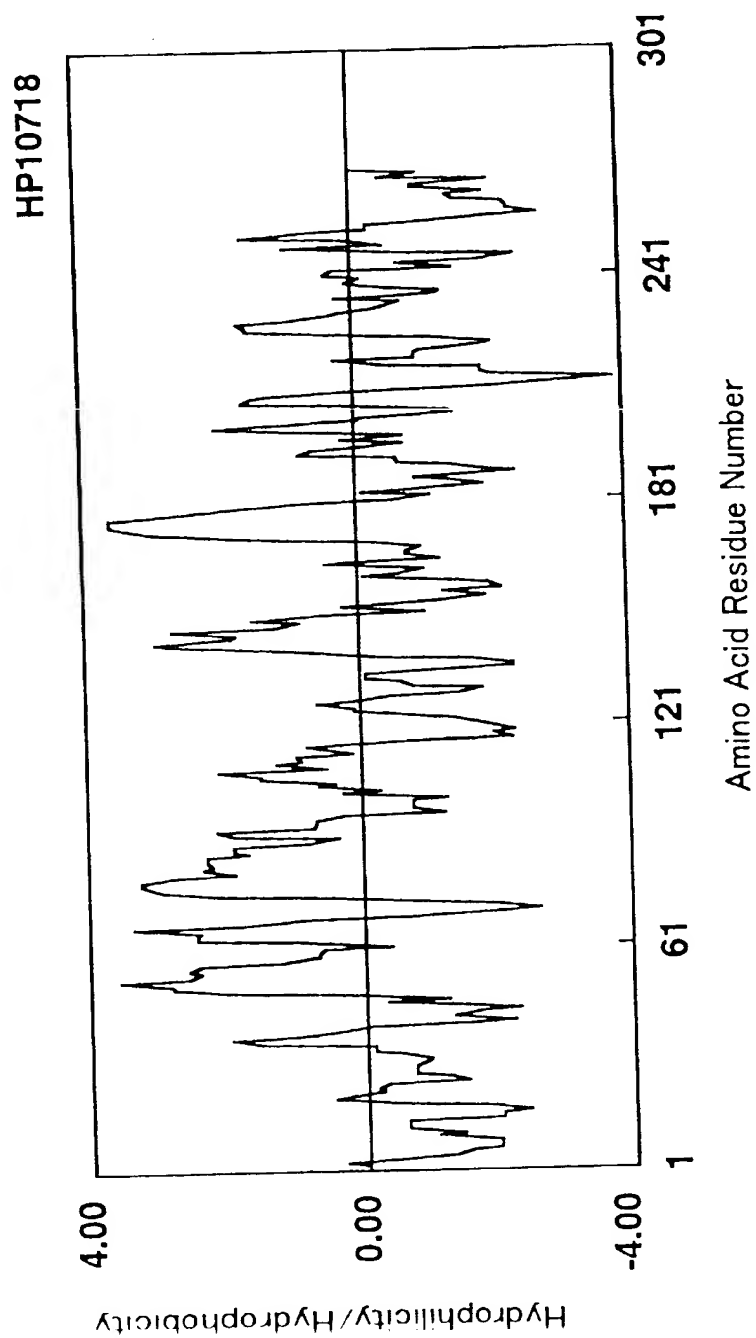


Fig.20

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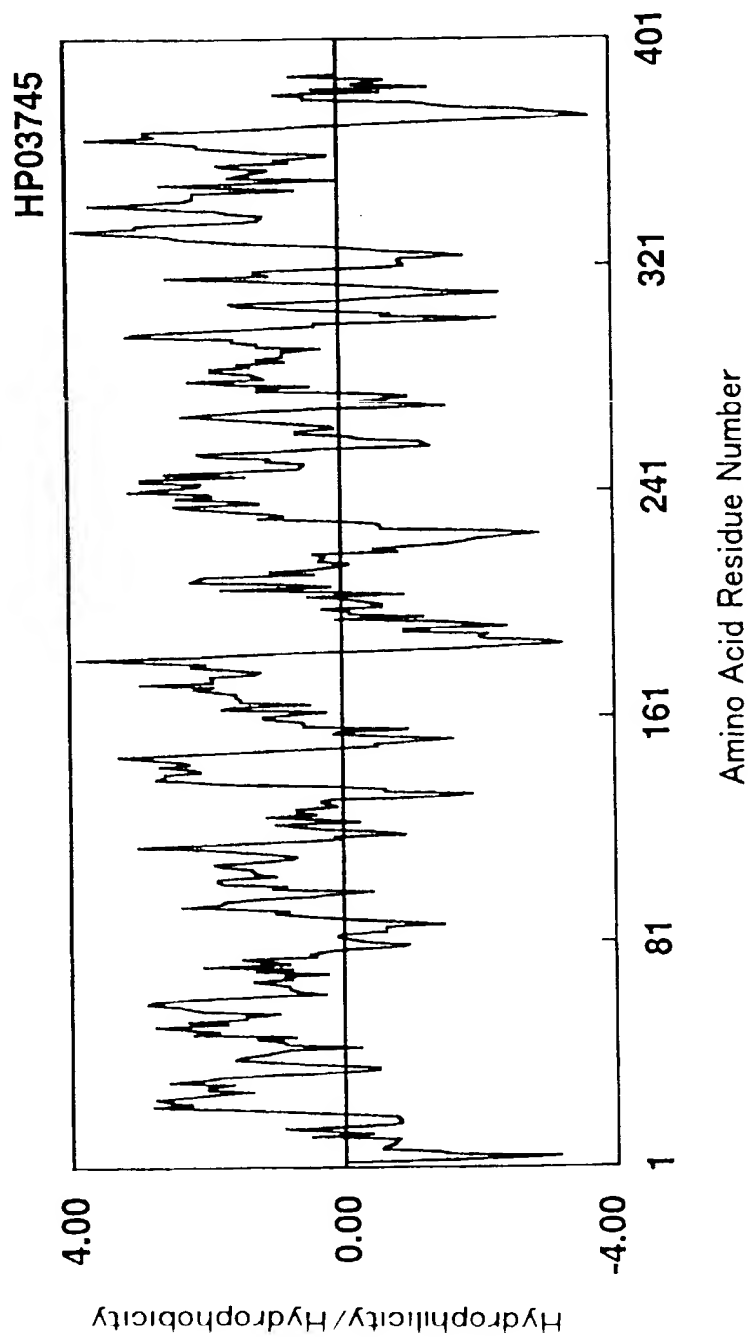


Fig.21

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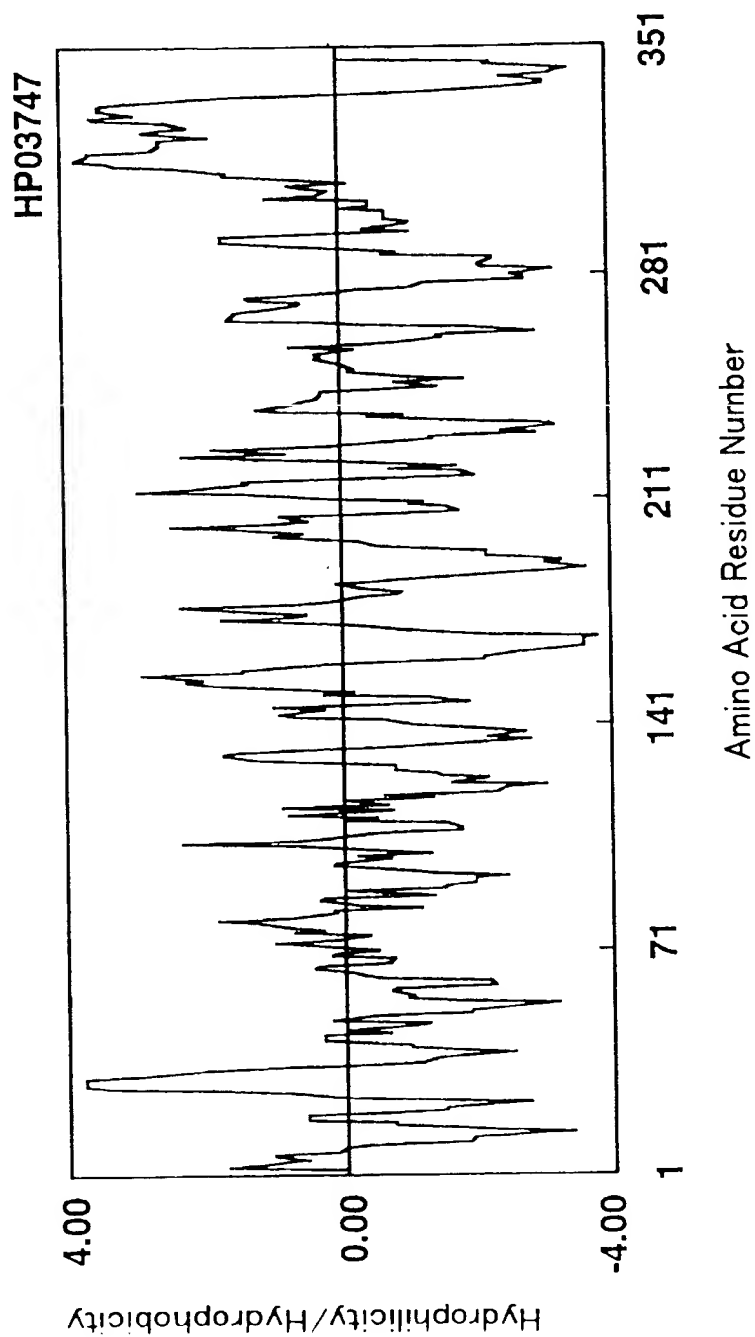


Fig.22

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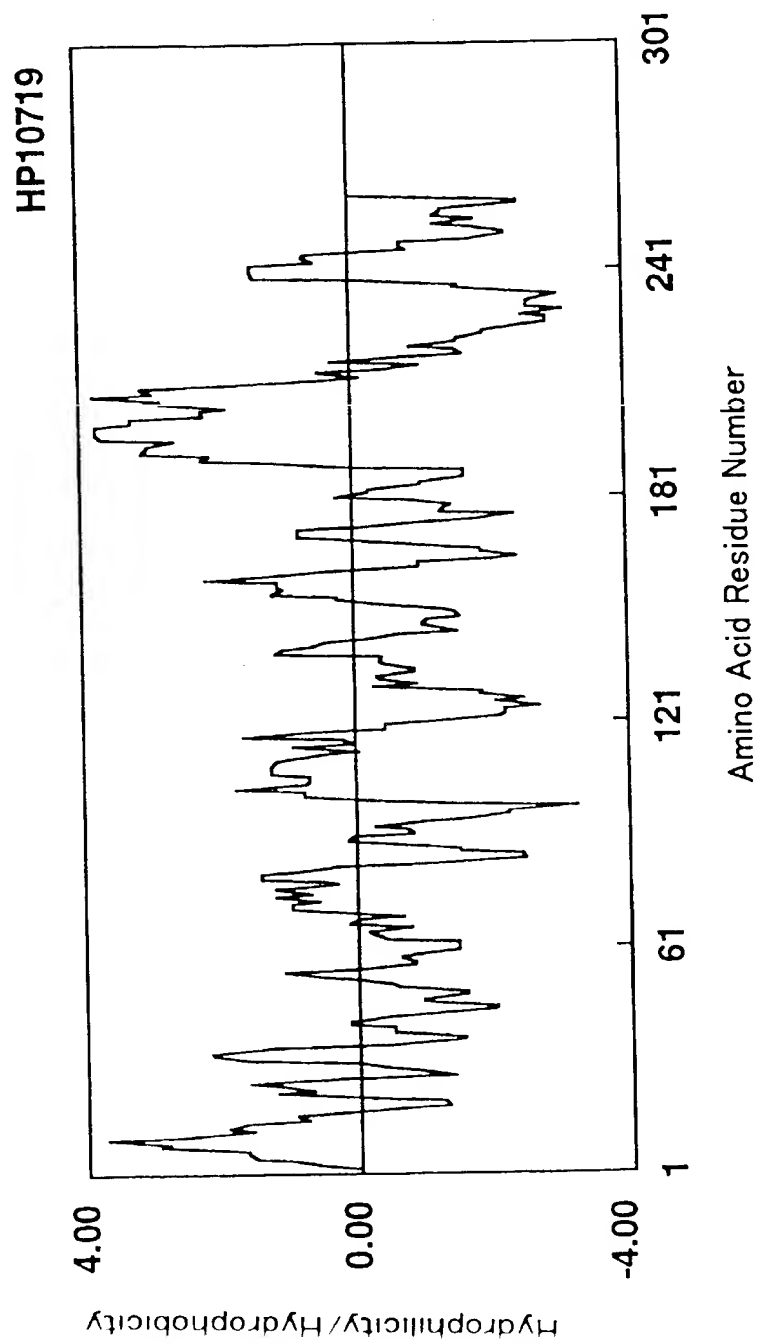


Fig.23

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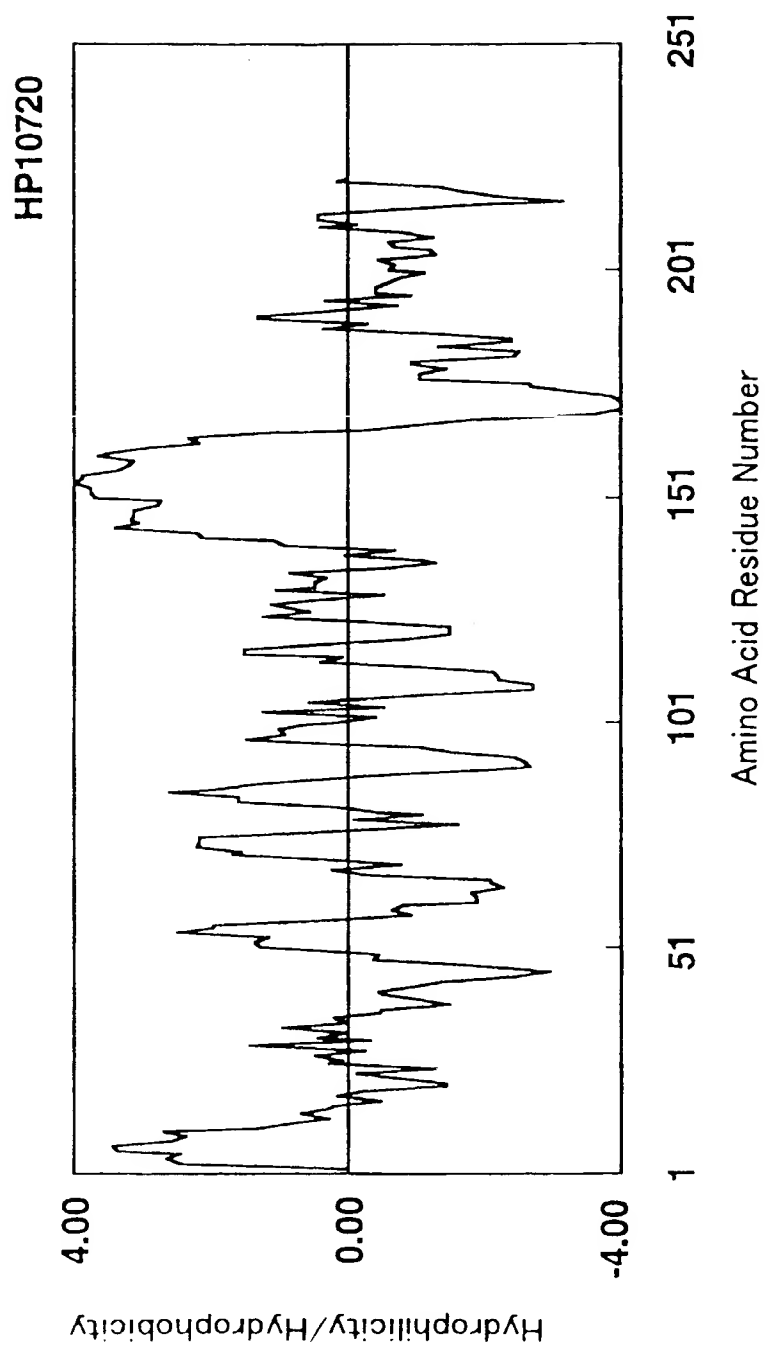


Fig.24

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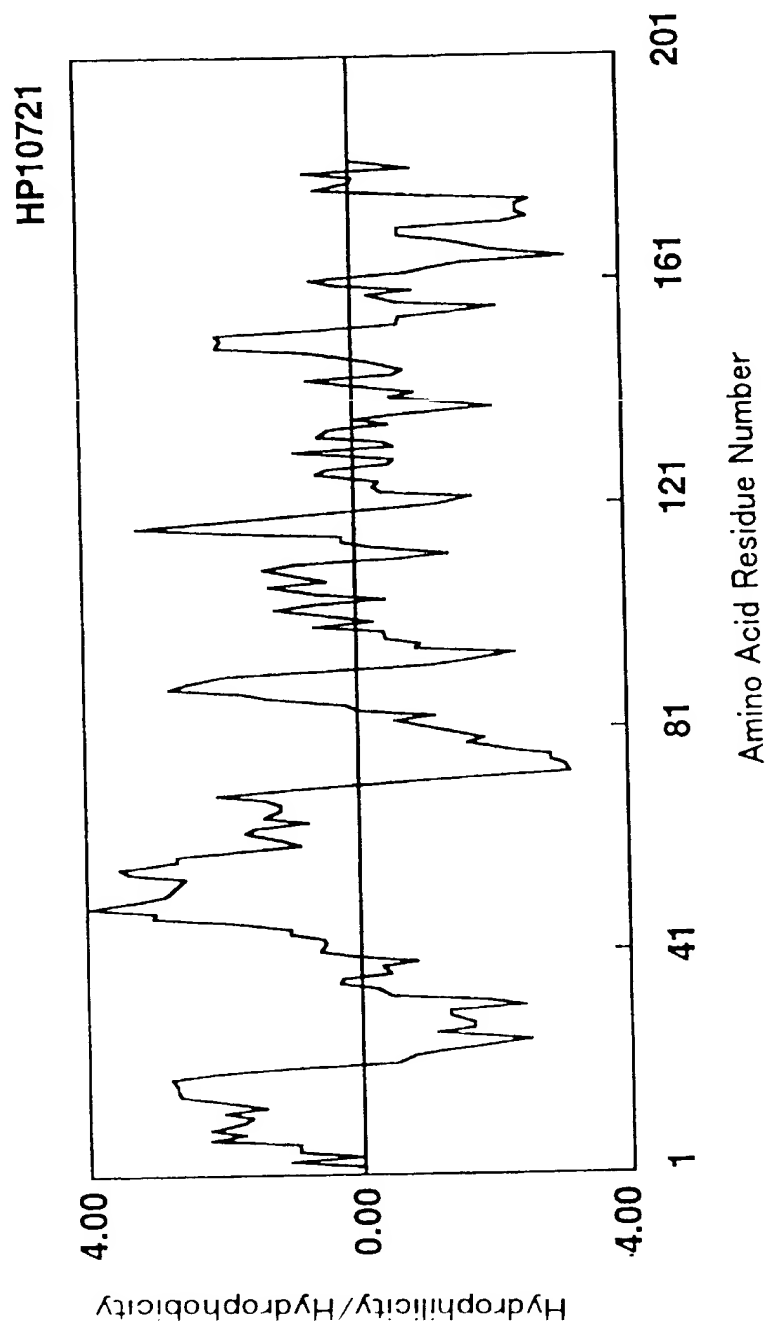


Fig.25

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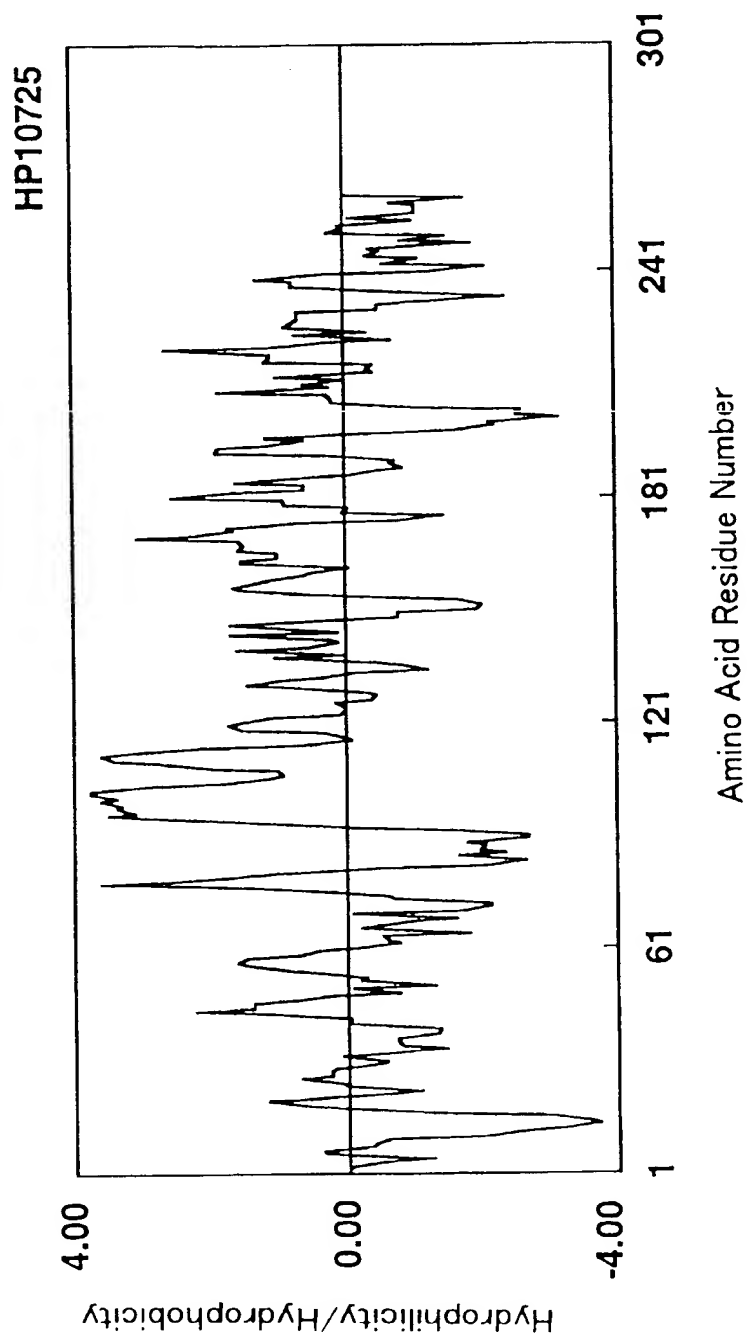


Fig.26

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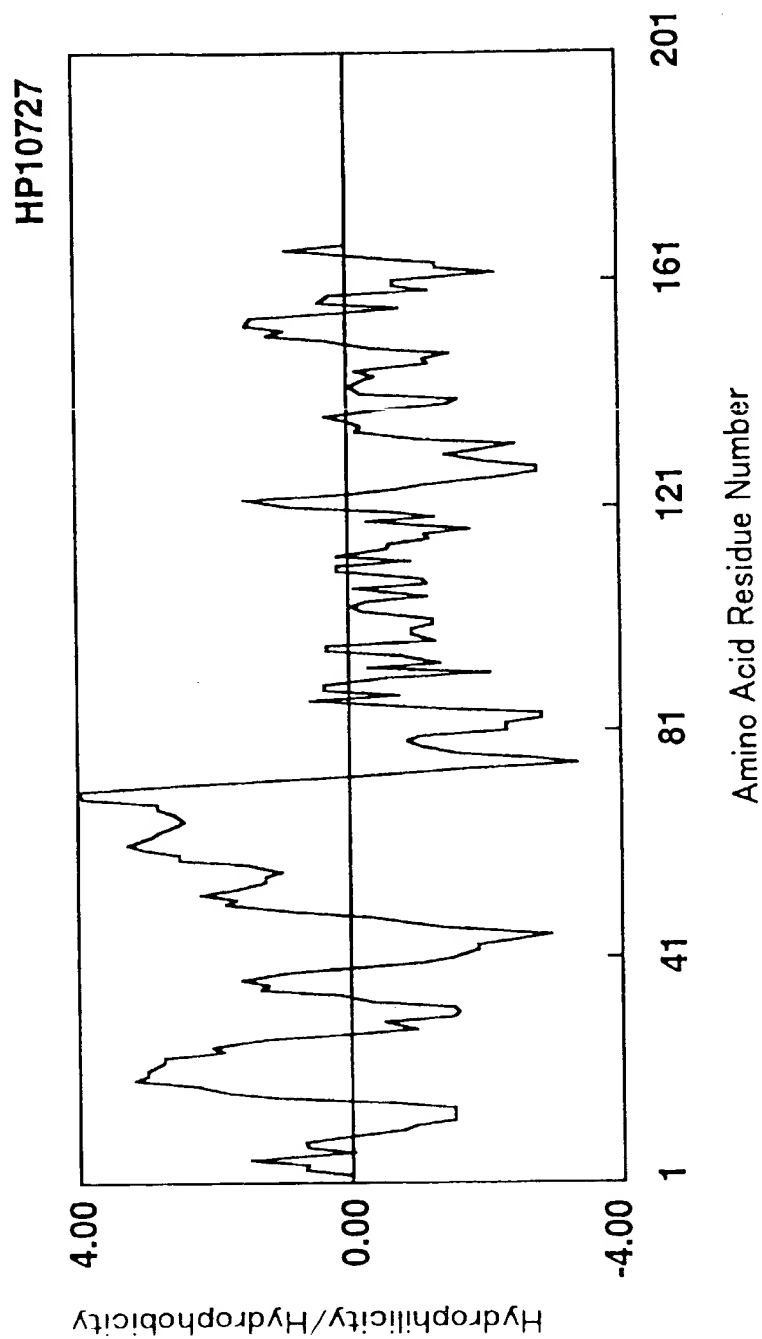


Fig.27



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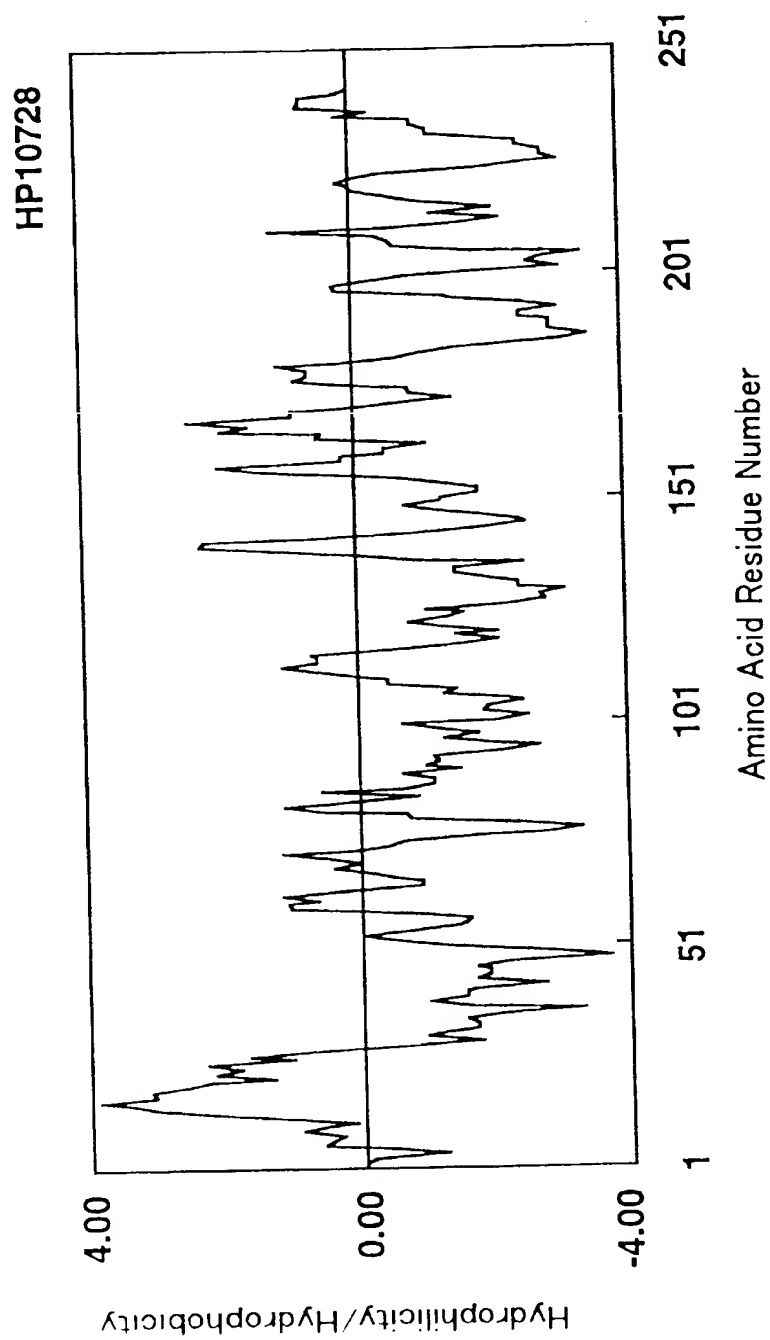


Fig.28

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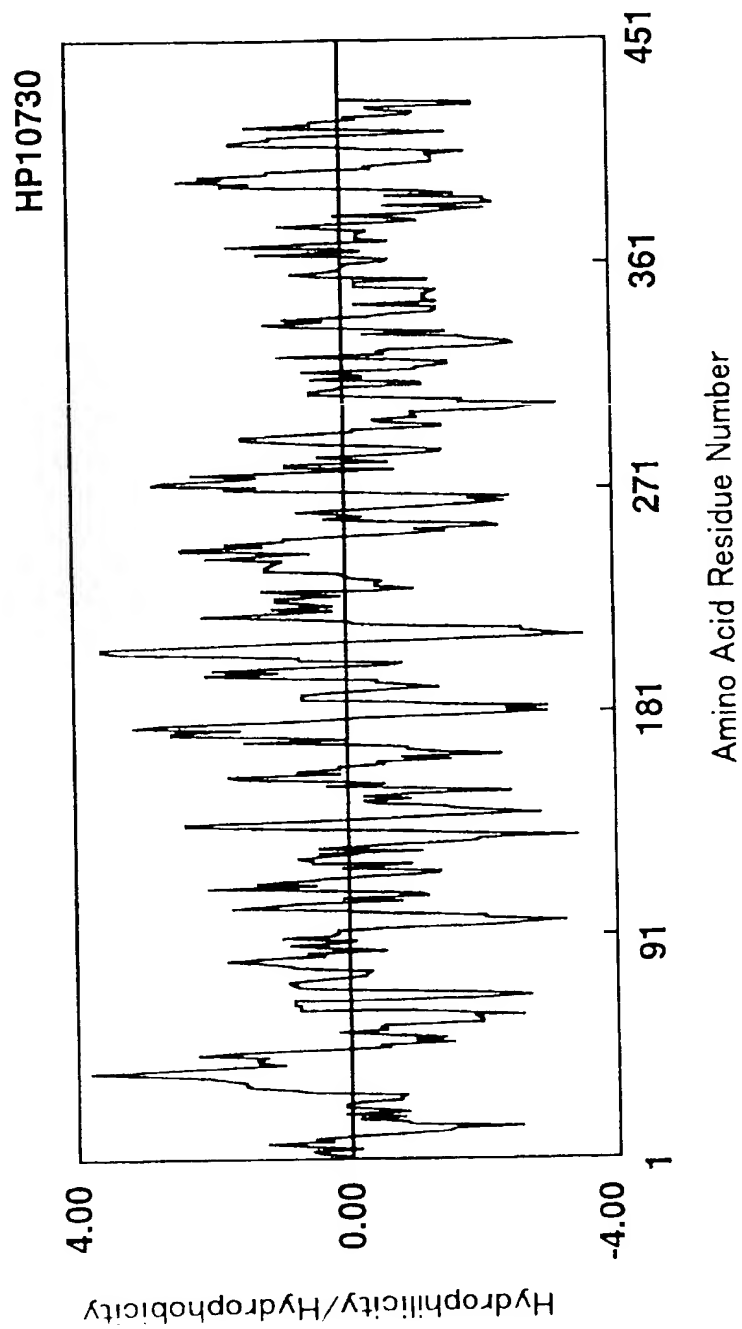


Fig.29

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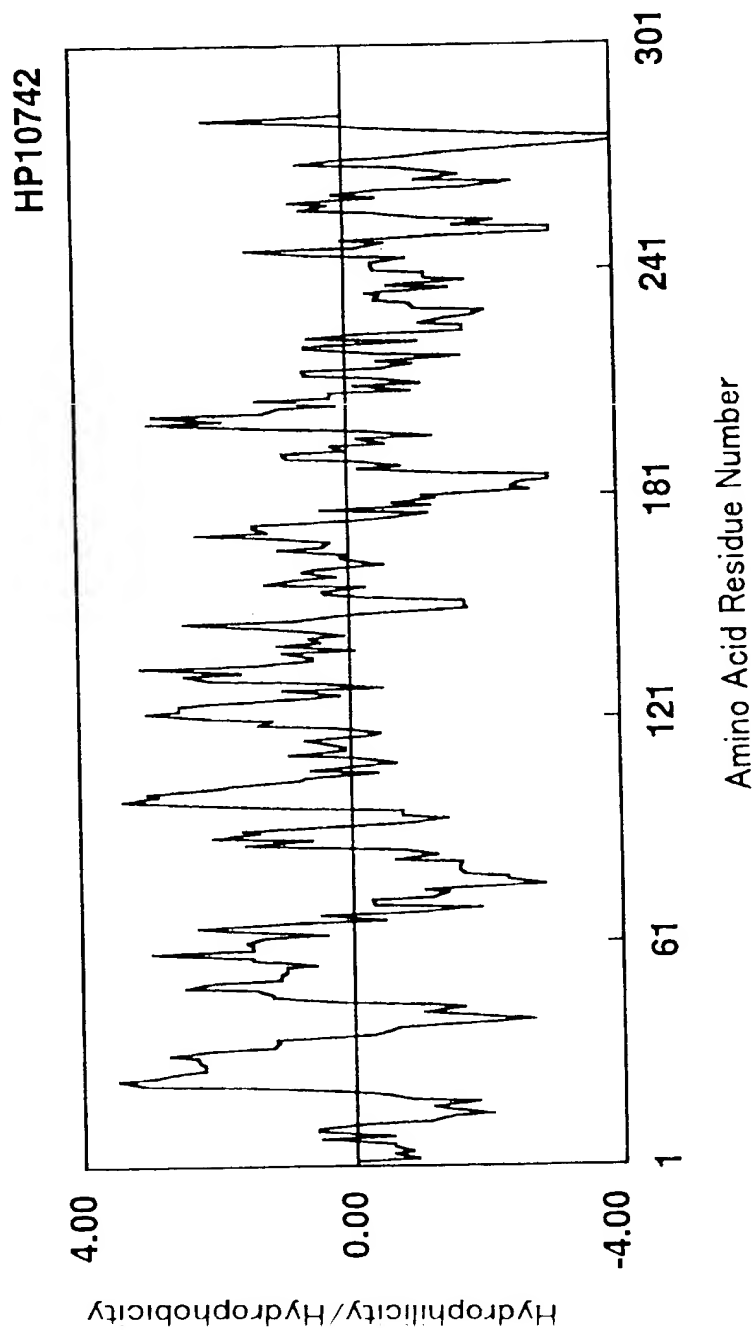


Fig.30

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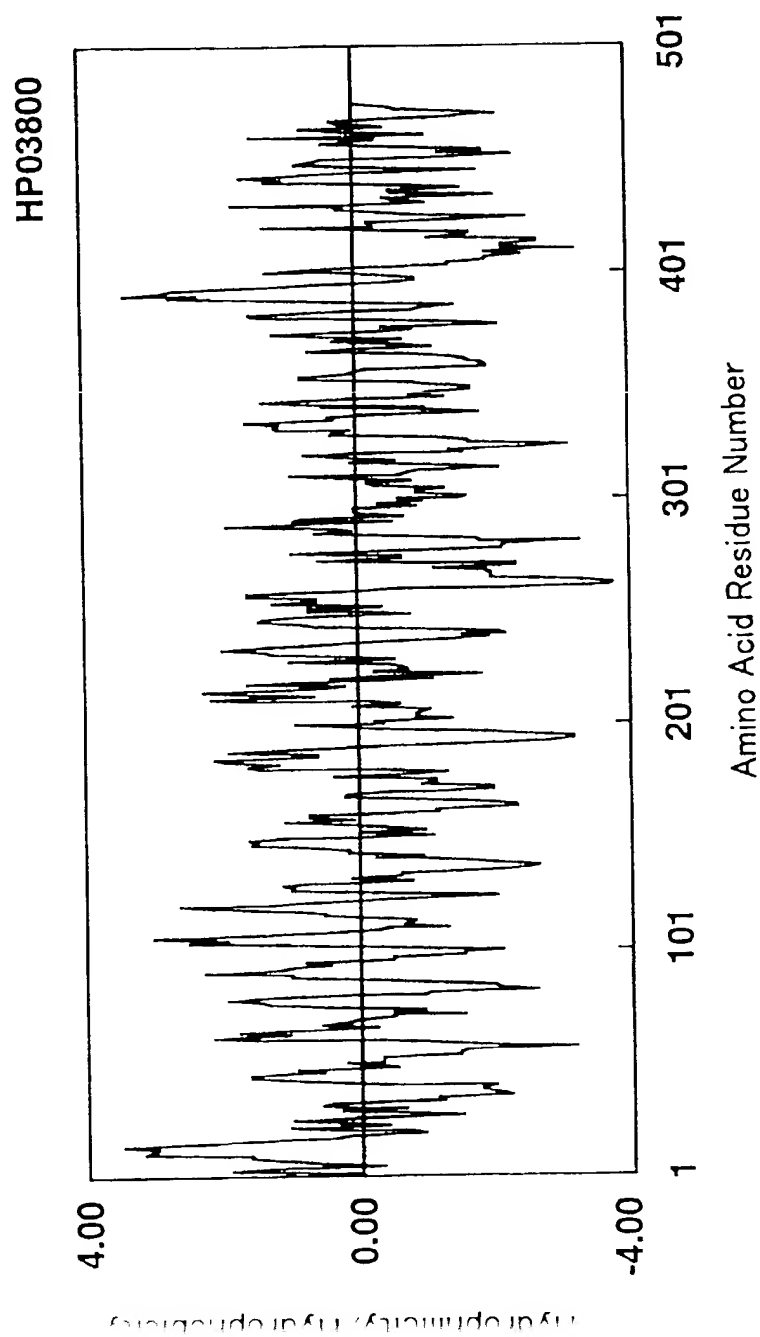


Fig.31

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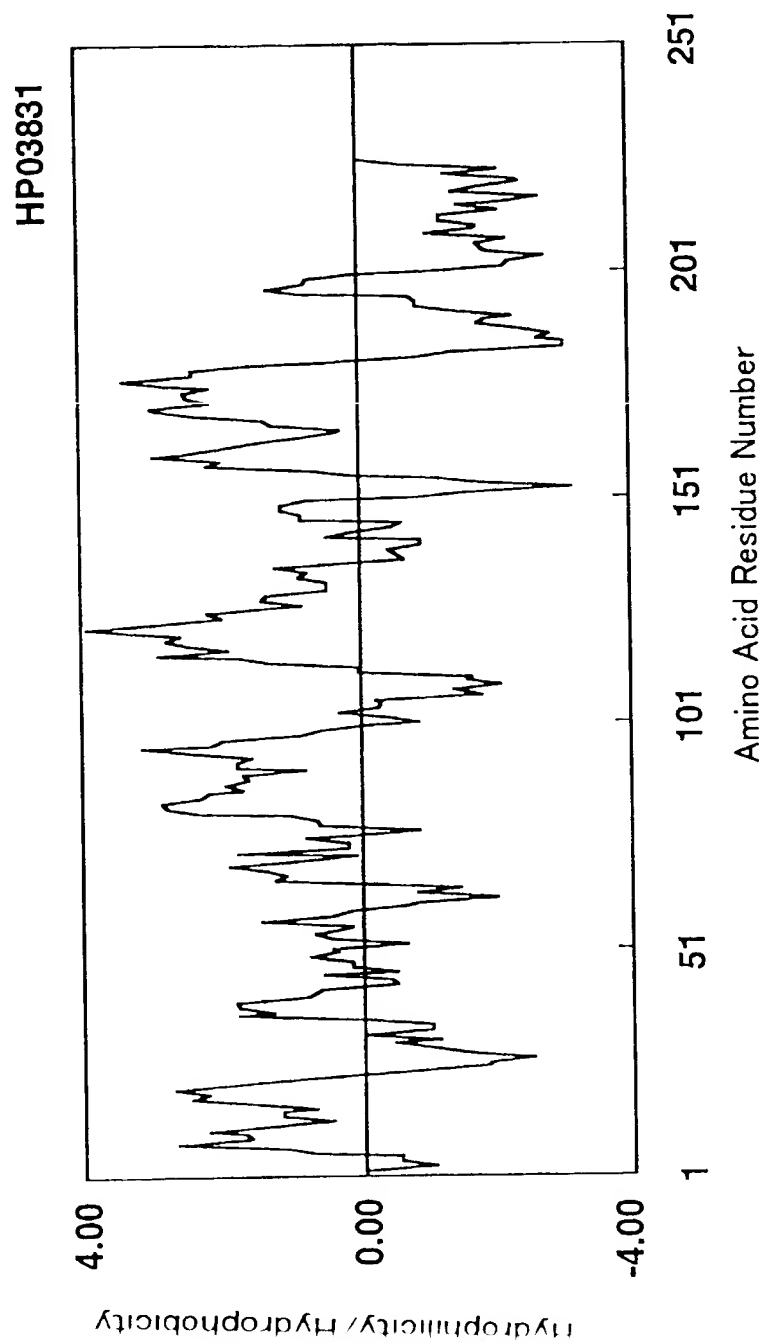


Fig.32

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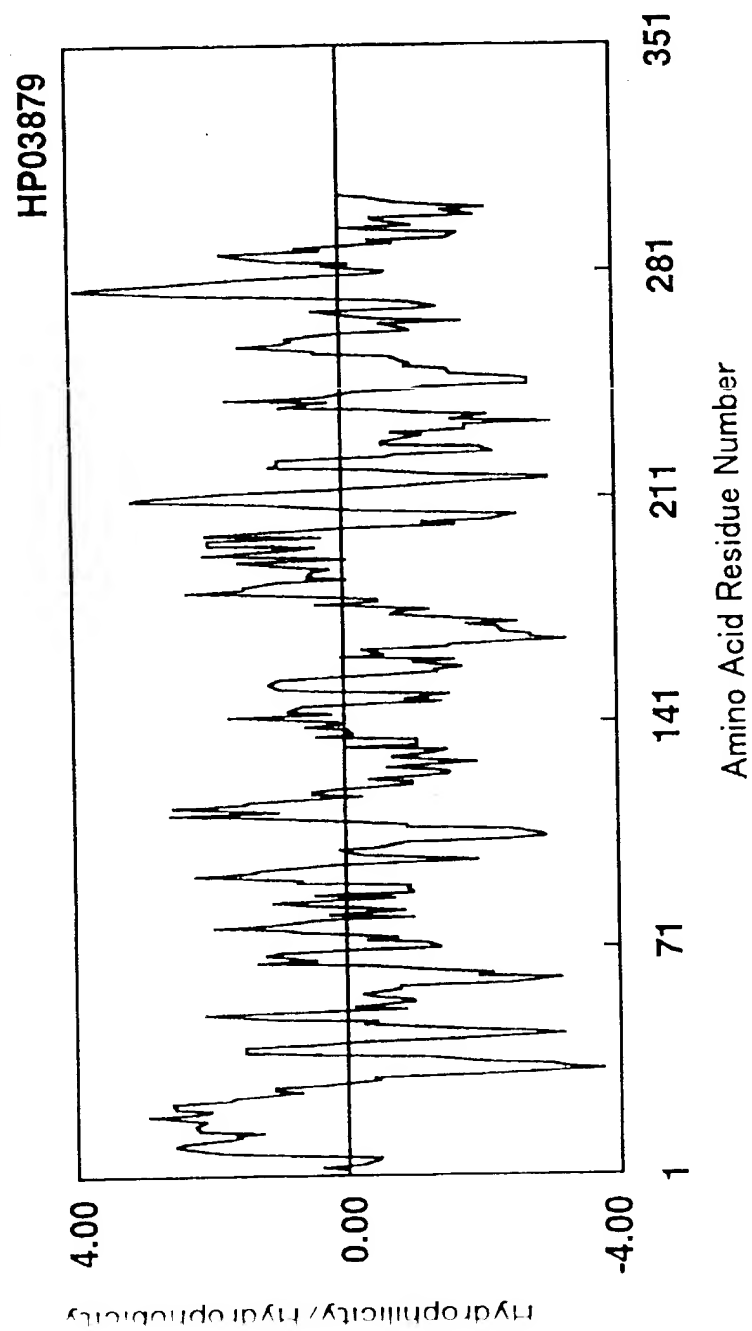


Fig.33

34/50

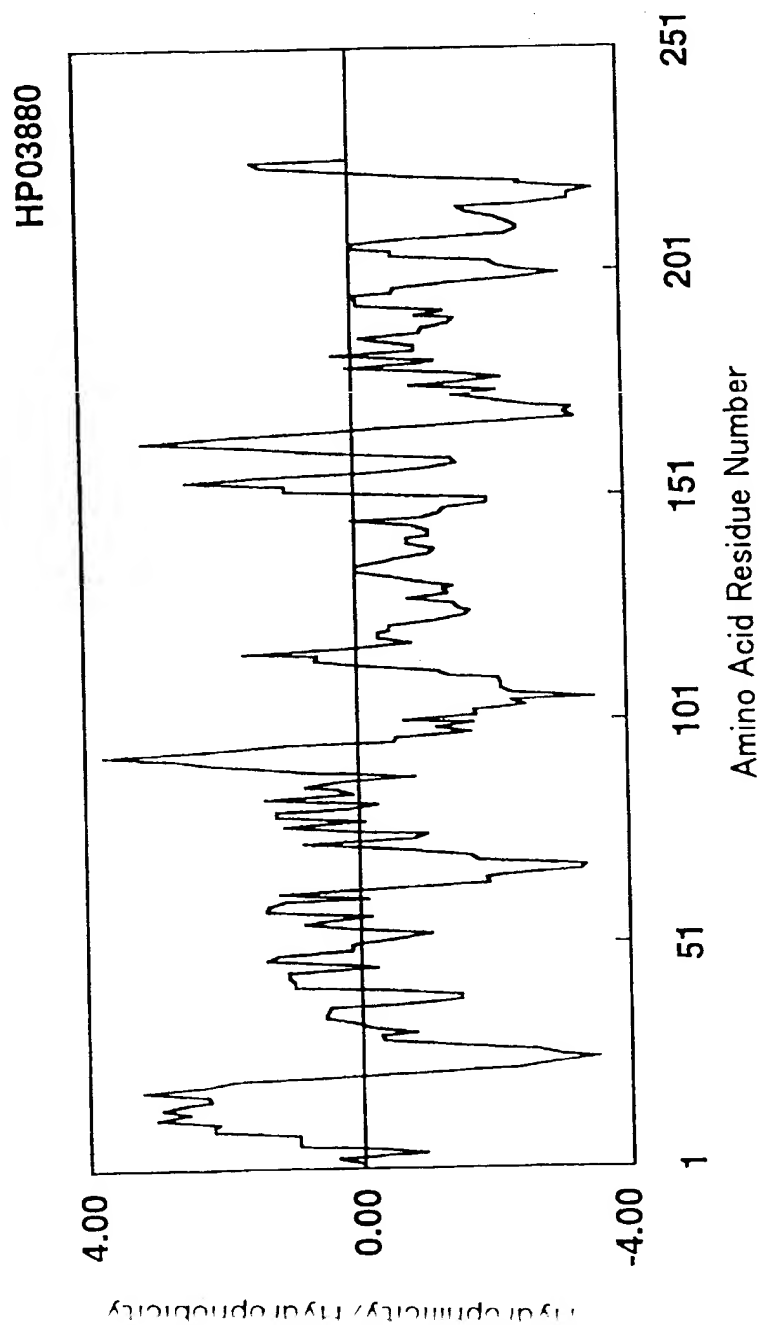


Fig.34

35/50

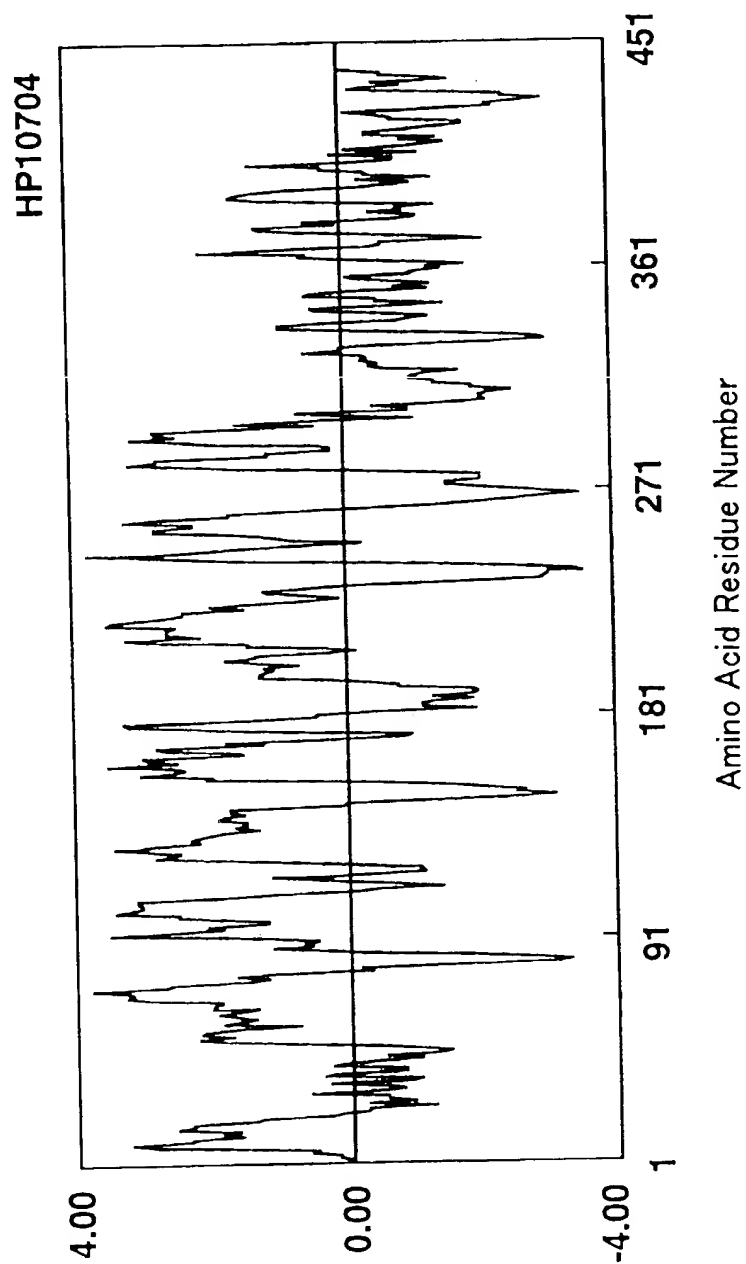


Fig.35



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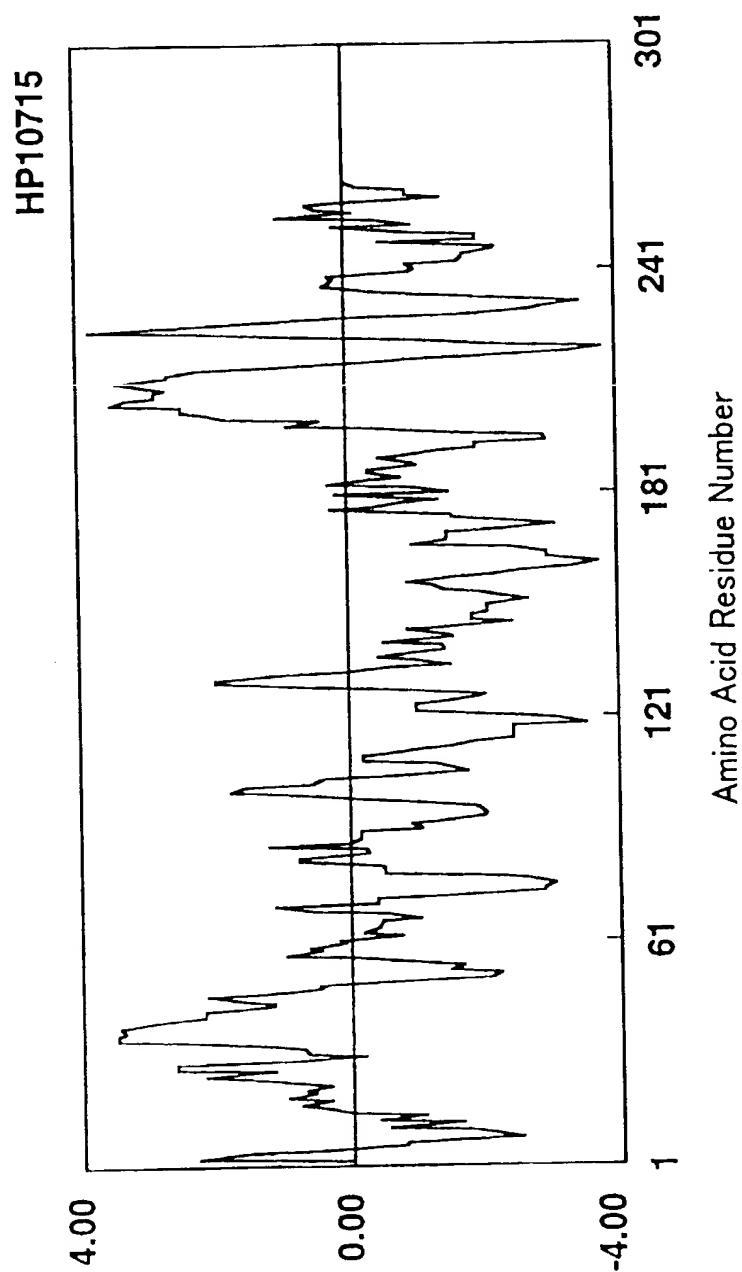


Fig.36

37/50

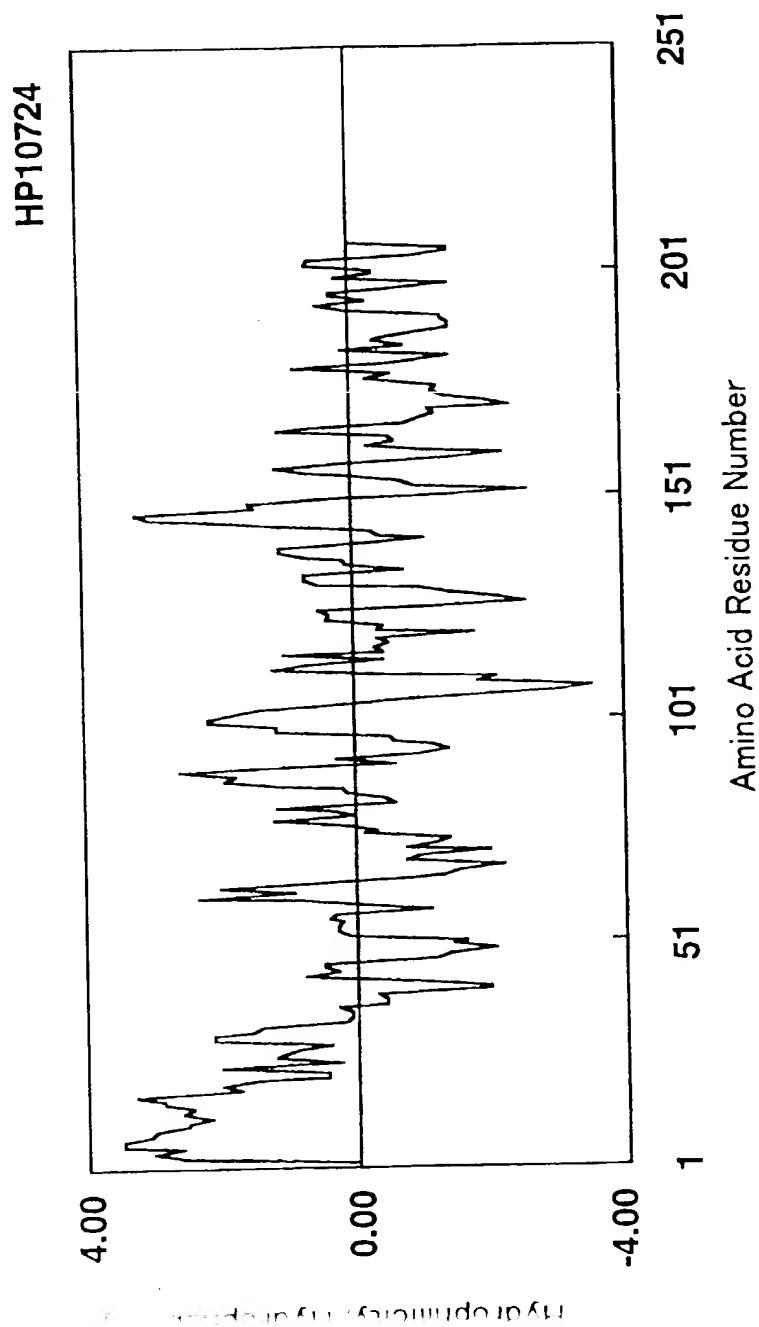


Fig.37

38/50

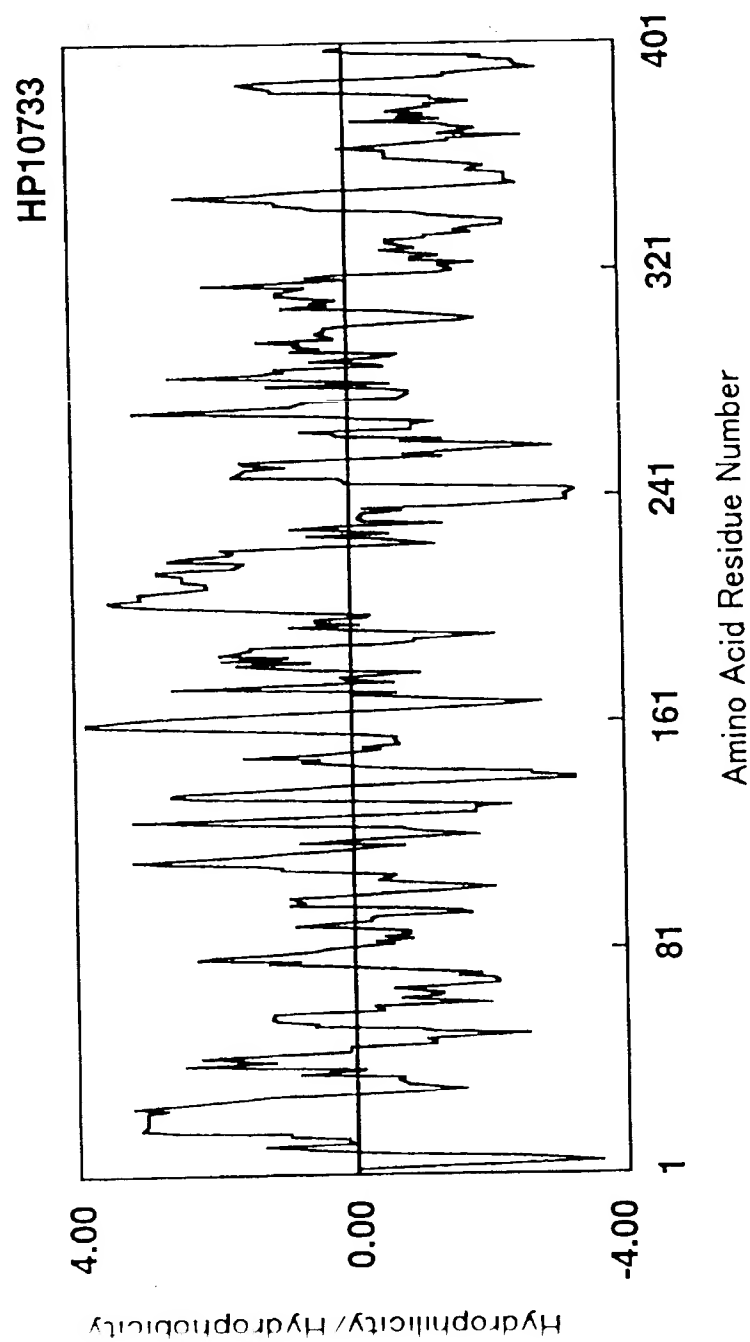


Fig.38

39/50

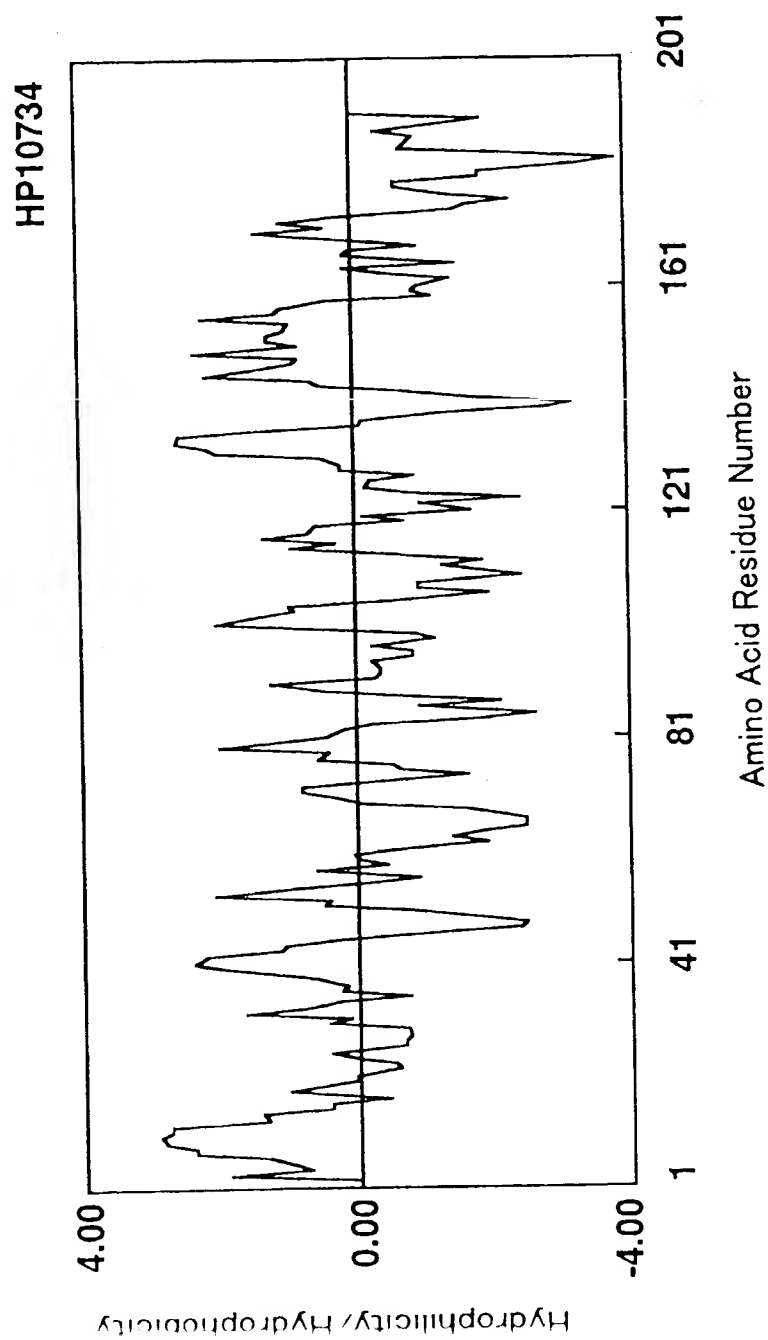


Fig.39

40/50

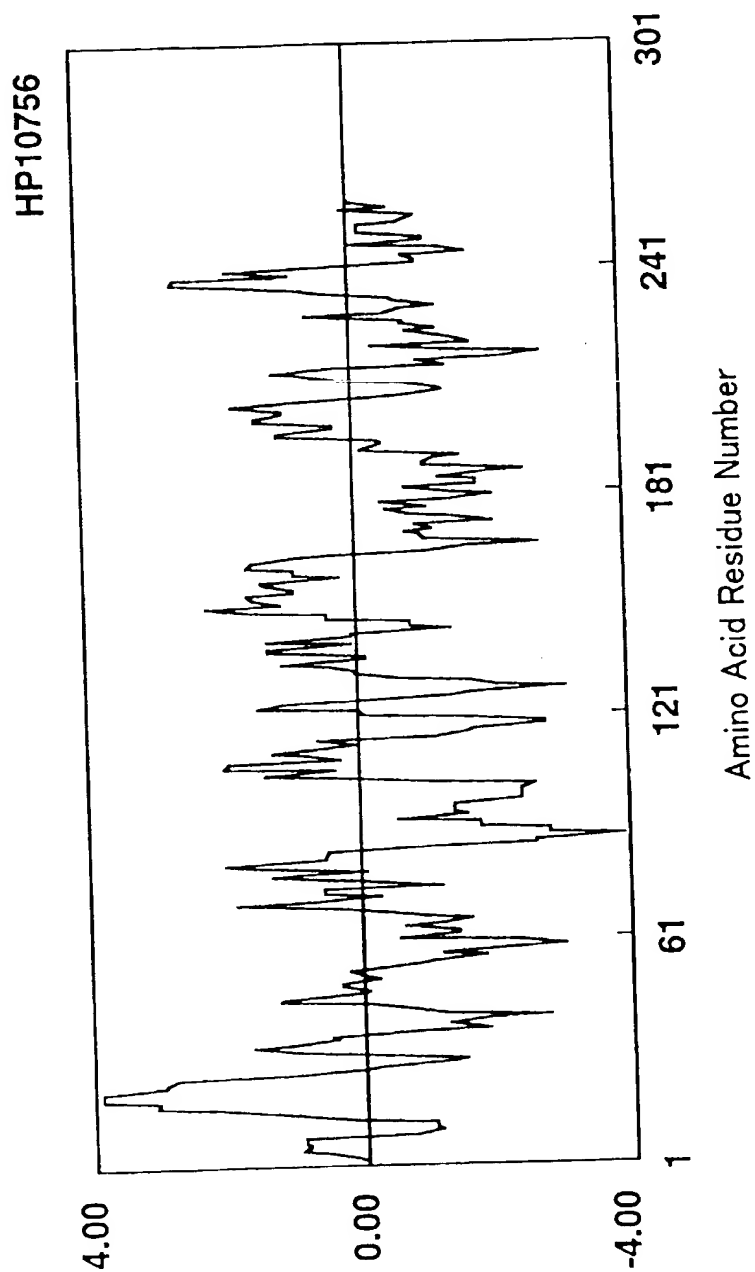


Fig.40

41/50

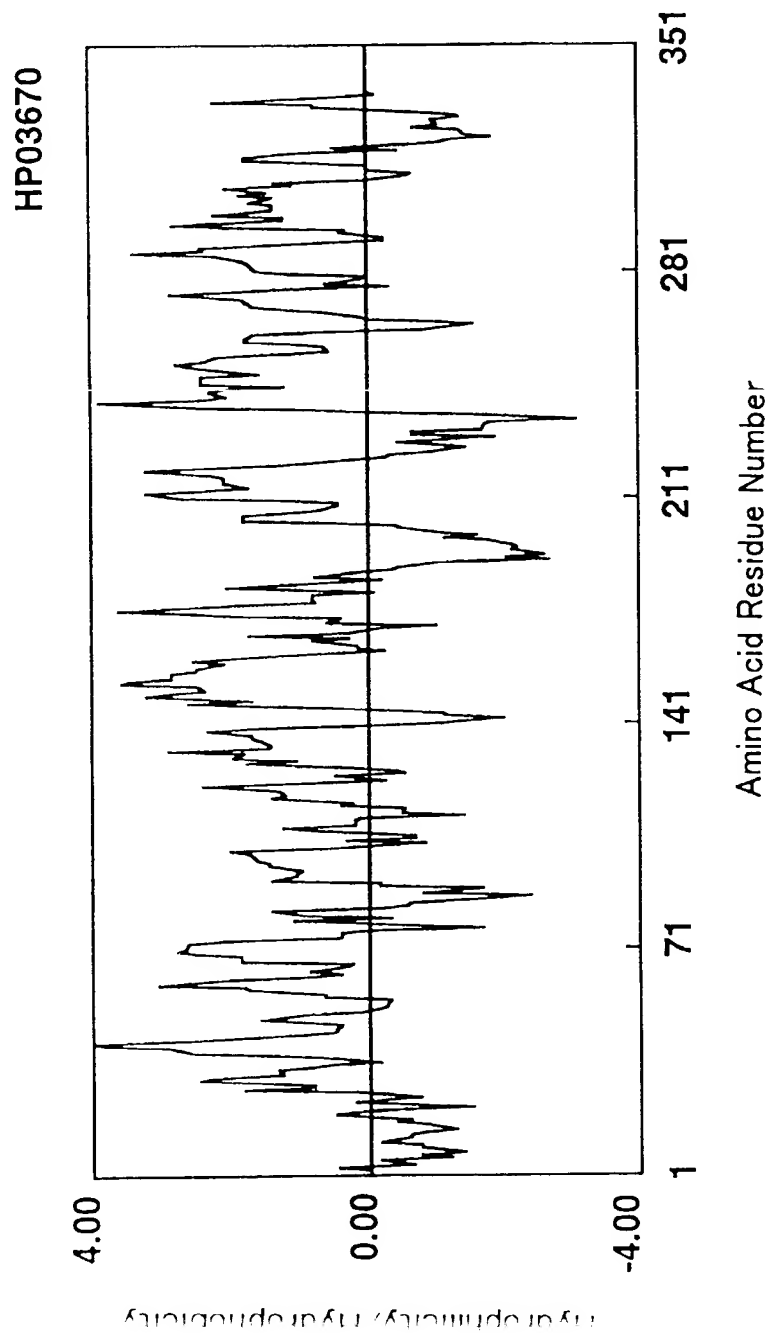


Fig.41

42/50

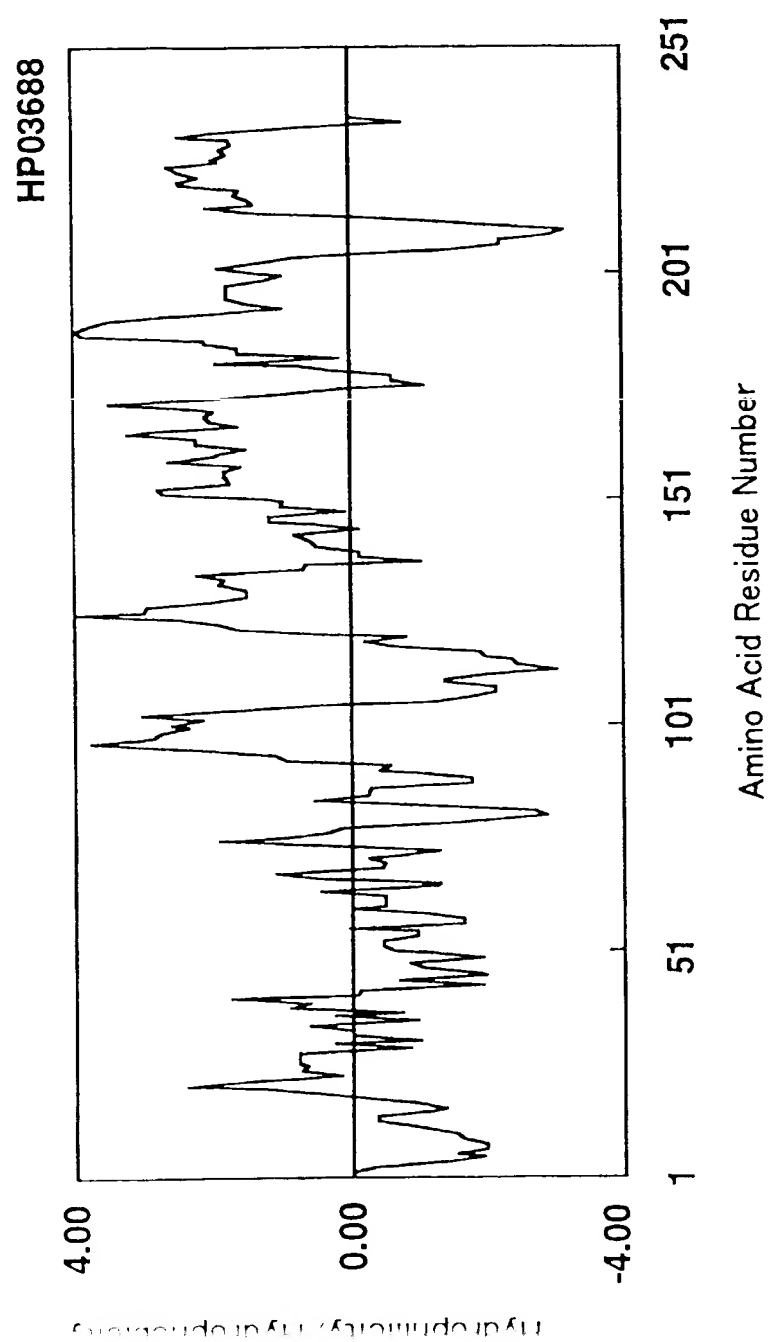


Fig.42

43/50

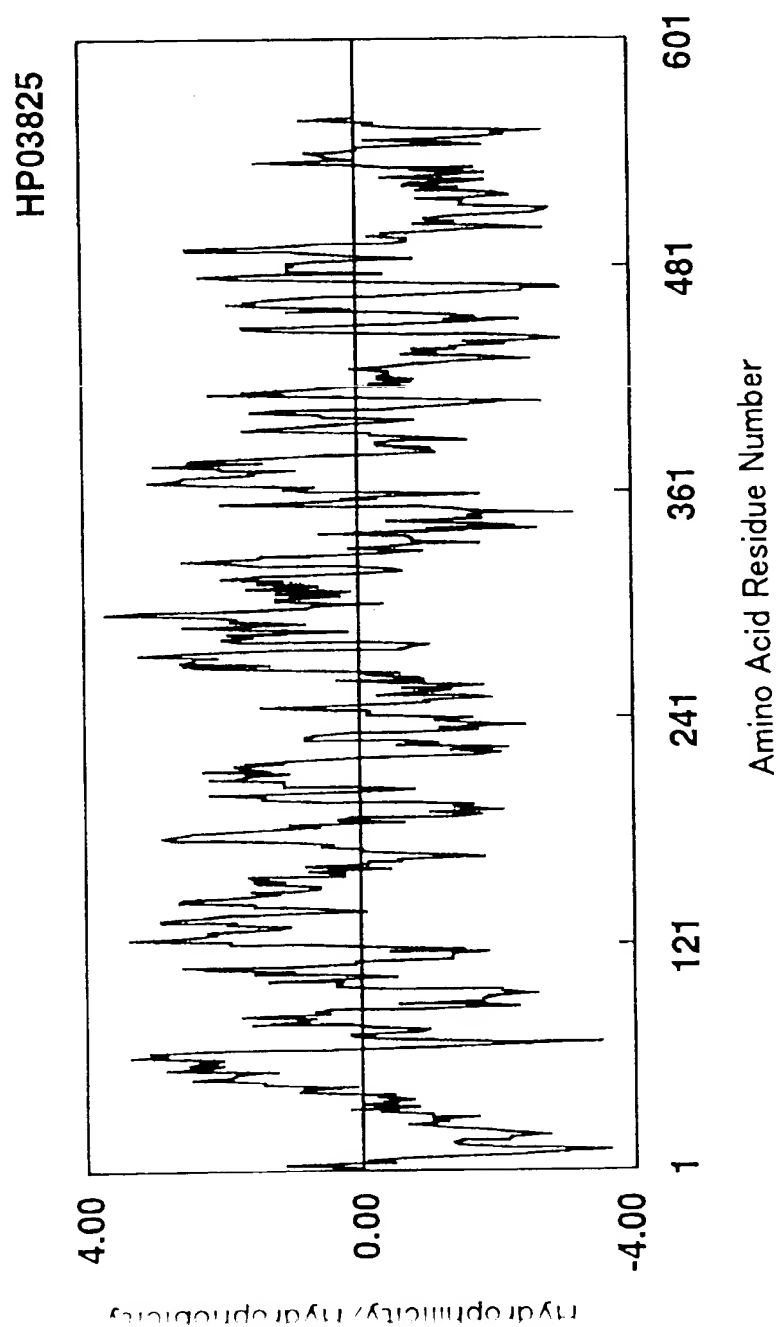


Fig.43



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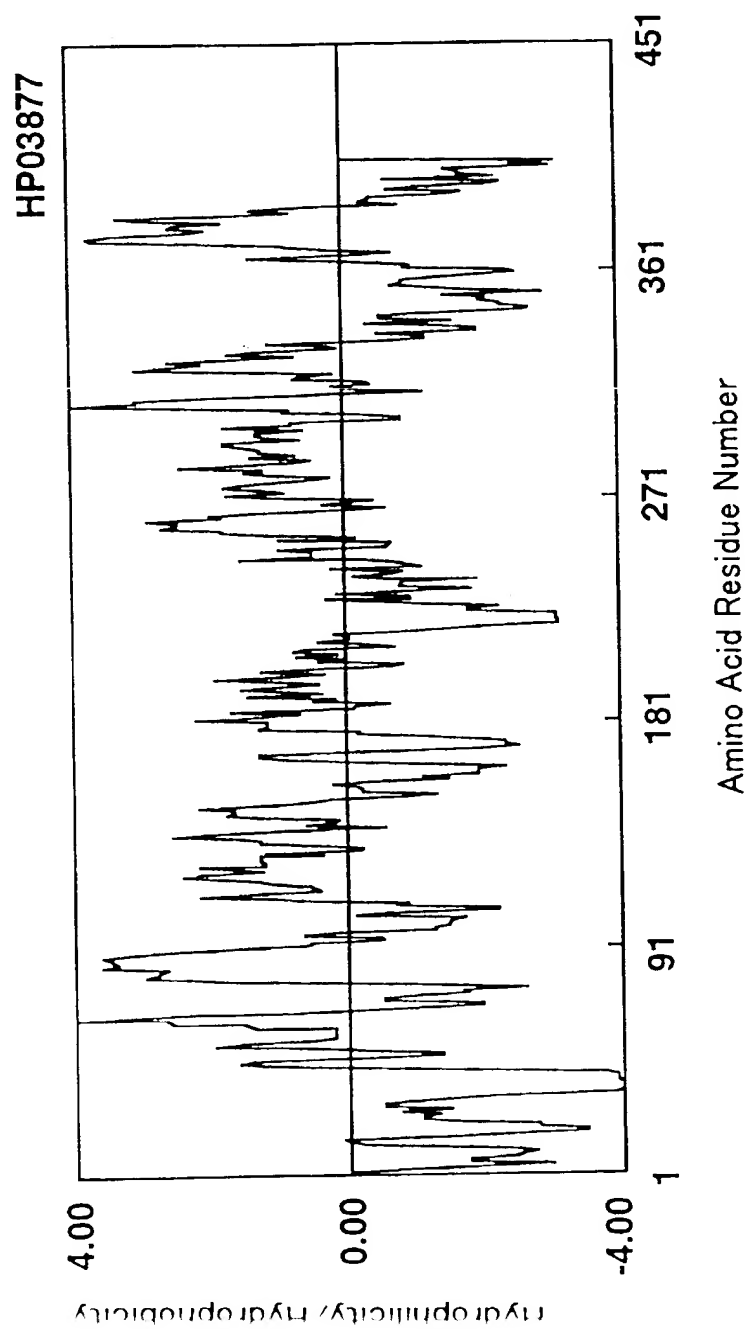


Fig.44

45/50

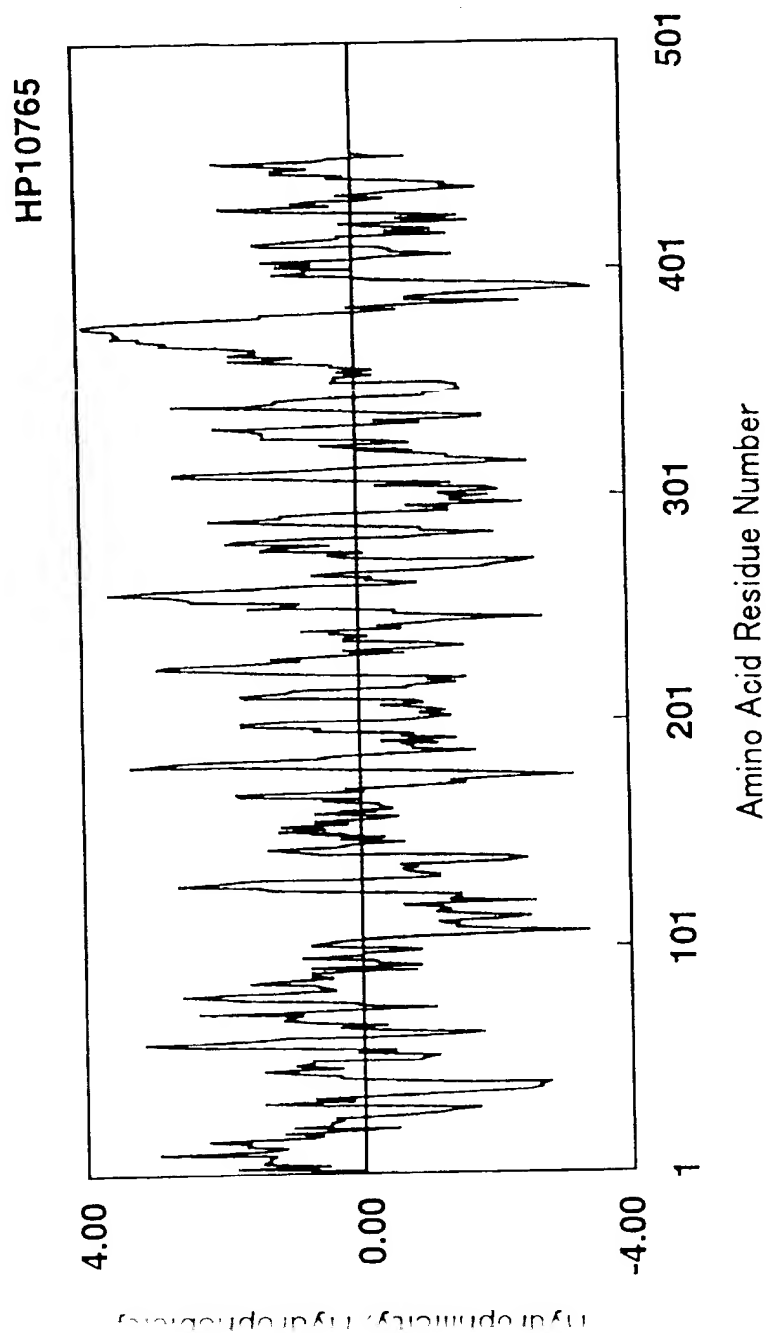


Fig.45

46/50

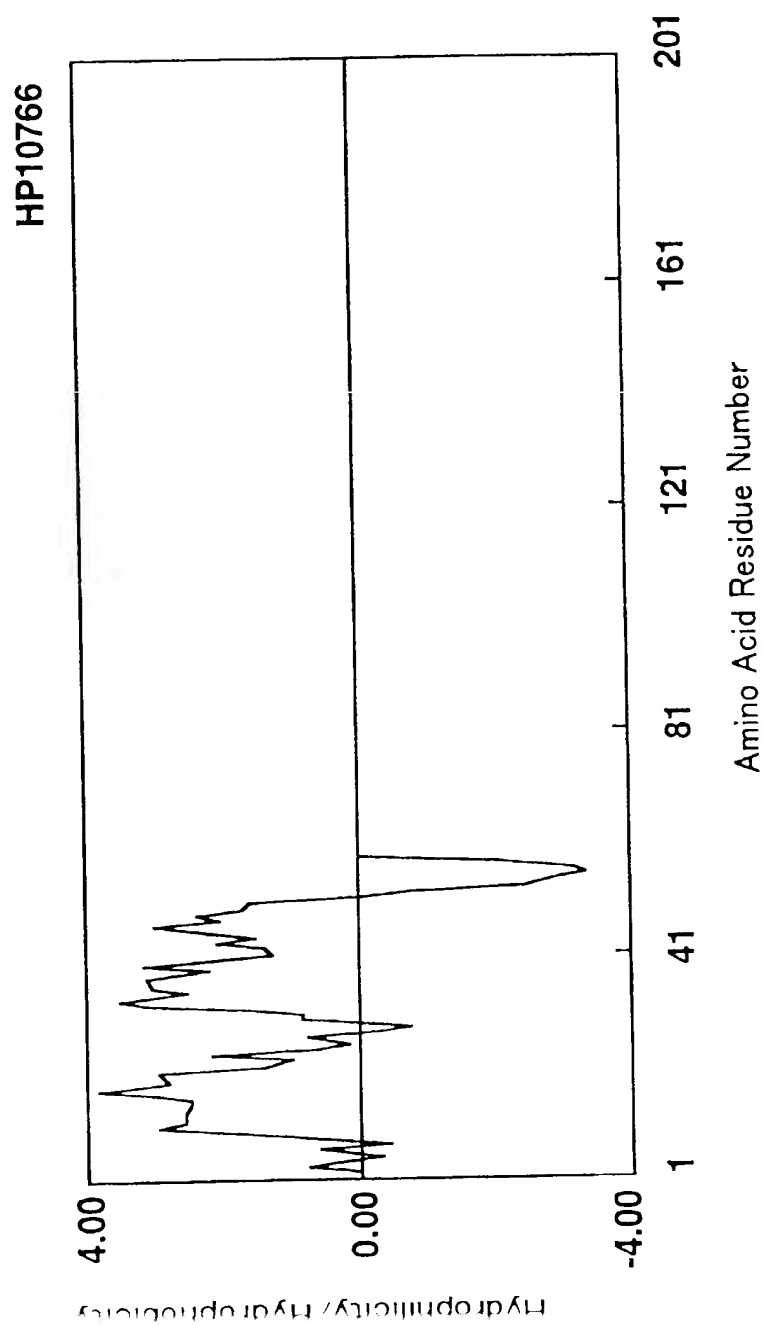


Fig.46

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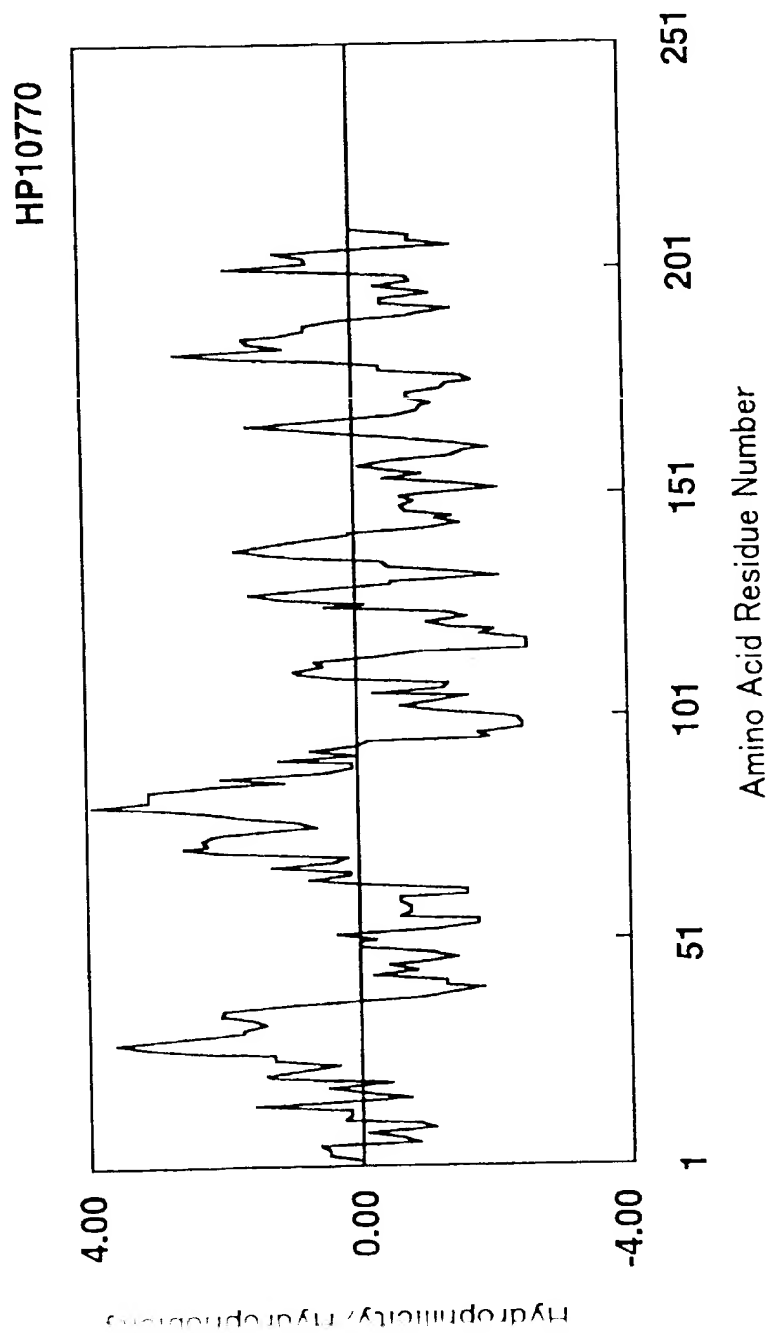


Fig.47

48/50

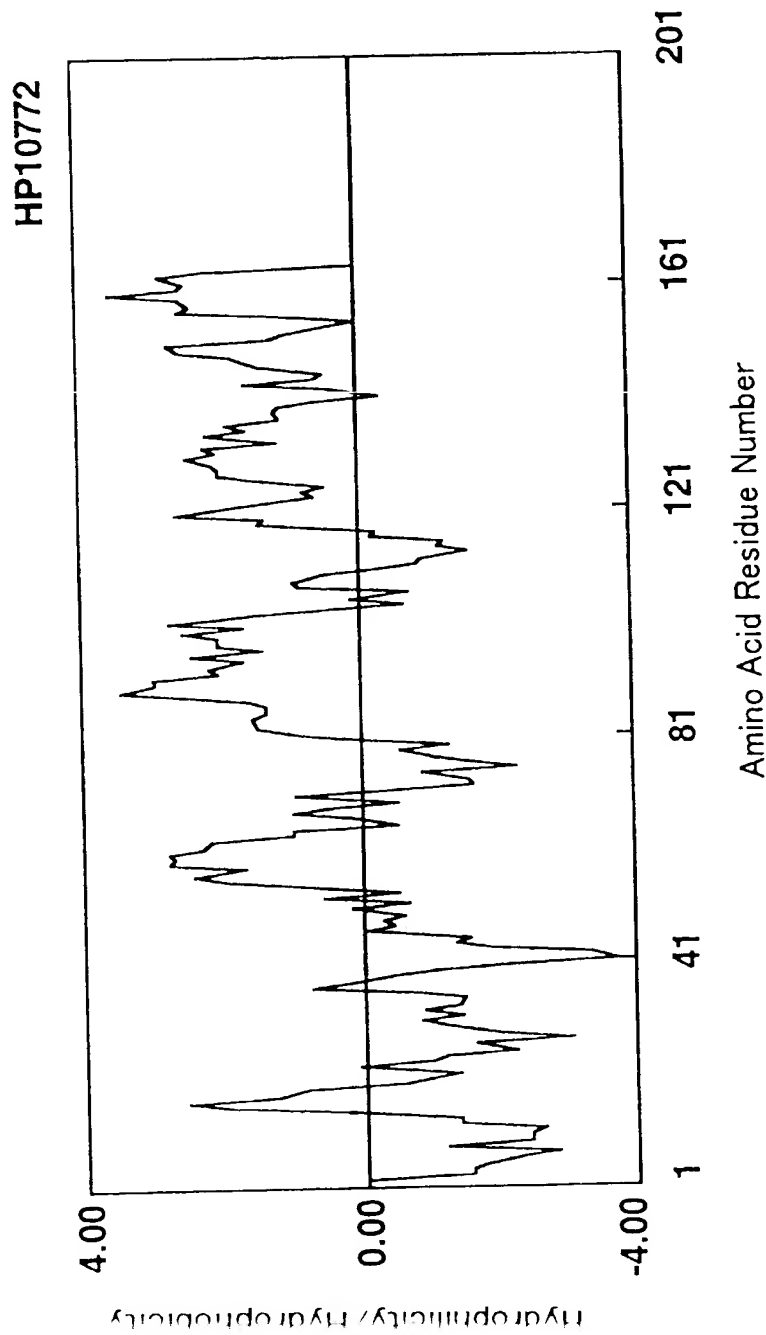


Fig.48

49/50

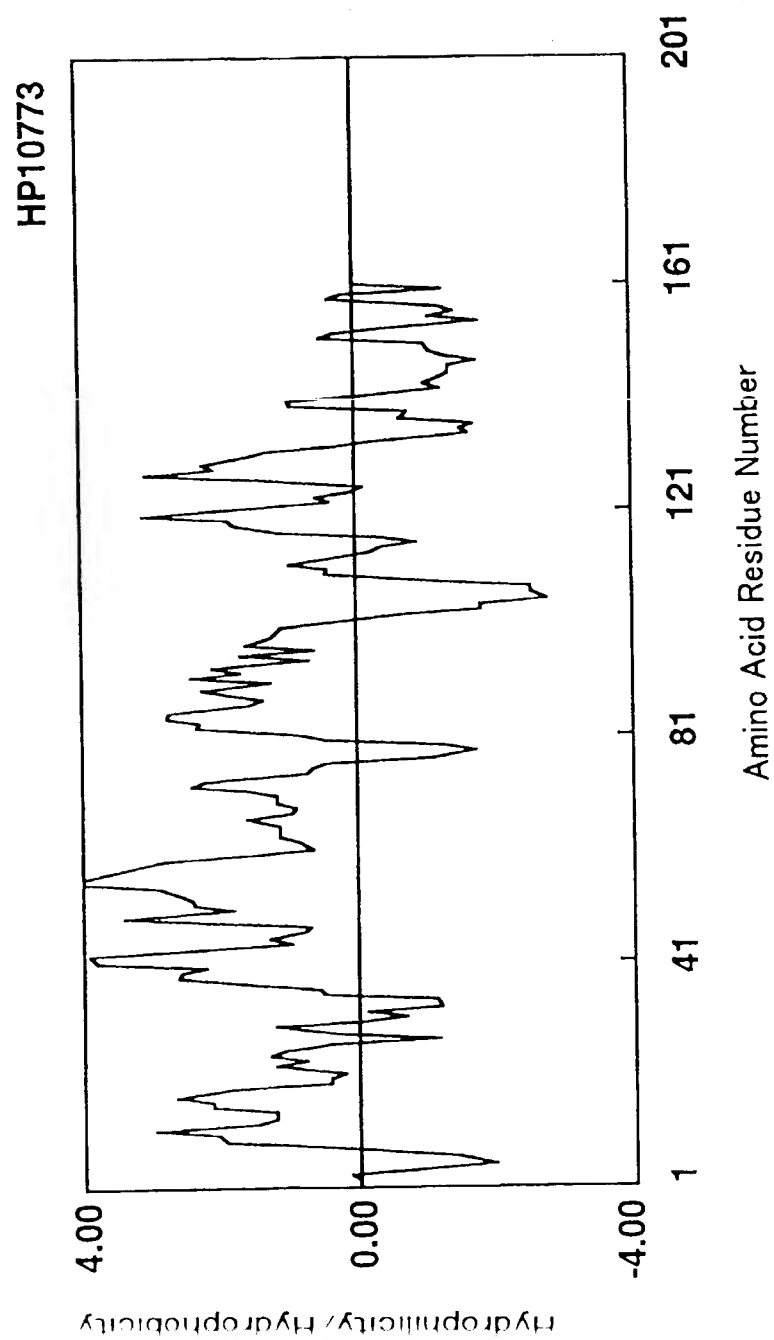


Fig.49

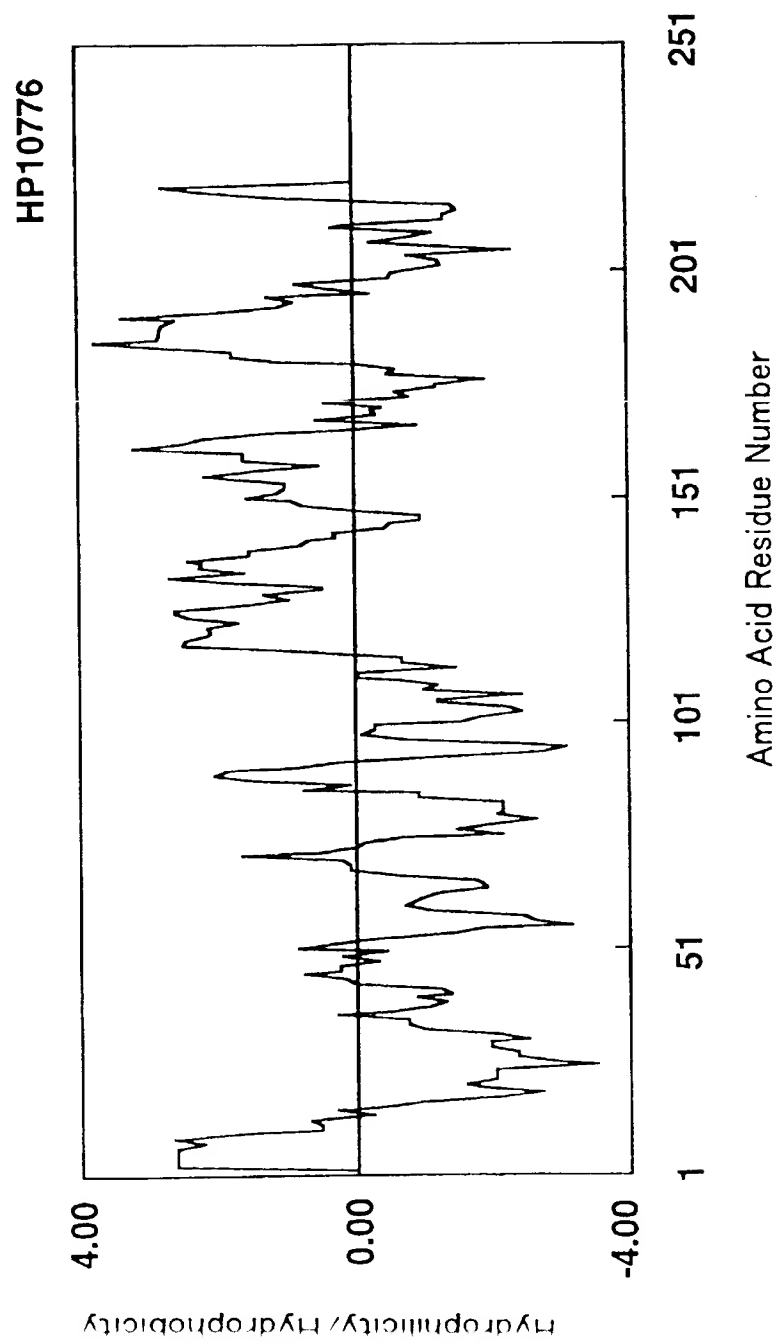


Fig.50

1 /307

## SEQUENCE LISTING

<110> Sagami Chemical Research Center,  
Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these  
proteins

<130> 662029

<150> JP 11-230344

<151> 1999-08-17

<150> JP 11-252551

<151> 1999-09-07

<150> JP 11-281132

<151> 1999-10-01

<150> JP 11-301624

<151> 1999-10-22

<150> JP 11-313877



2 /307

&lt;160&gt; 150

&lt;210&gt; 1

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Met Val Lys Ile Ser Phe Gln Pro Ala Val Ala Gly Ile Lys Gly Asp

1 5 10 15

Lys Ala Asp Lys Ala Ser Ala Ser Ala Pro Ala Pro Ala Ser Ala Thr

20 25 30

Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg

35 40 45

Ser Lys Arg Gly Ser Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly

50 55 60

Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr

65 70 75 80

Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys

85 90 95

Gly Val Leu Tyr Glu Asp Ser Leu Ser Ser Gln Val Arg Thr Gln Met

100 105 110

Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg

130

135

140

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Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Ser Leu

145 150 155 160

Asp Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro

165 170 175

Arg Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu

180 185 190

Pro Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val

195 200 205

Ser Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly

210 215 220

Lys Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn

225 230 235 240

Lys Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr

245 250 255

Phe Val Val Glu Thr Leu Ile Cys Gly Val Val

260 265

&lt;210&gt; 2

&lt;211&gt; 419

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

.....

Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala Ser Gln

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20	25	30	
Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro Gly Arg			
35	40	45	
Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly Leu Asp			
50	55	60	
Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu Pro Leu			
65	70	75	80
His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe			
85	90	95	
Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn			
100	105	110	
Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val			
115	120	125	
Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met			
130	135	140	
Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu			
145	150	155	160
Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln			
165	170	175	
Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg			
180	185	190	
Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile			

.....

210	215	220
-----	-----	-----

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Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys  
225 230 235 240  
Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu  
245 250 255  
Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys  
260 265 270  
Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys  
275 280 285  
Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys  
290 295 300  
Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro Cys  
305 310 315 320  
Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln Ala  
325 330 335  
Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser Leu  
340 345 350  
Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln Asp  
355 360 365  
Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr Lys  
370 375 380  
Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr Leu  
385 390 395 400  
Glu Trp Phe

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&lt;210&gt; 3

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Ala Ala

1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr

20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly

35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu

65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly

85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro

100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser

115 120 125

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg

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145                      150                      155                      160  
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
                         165                      170                      175  
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
                         180                      185                      190  
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
                         195                      200                      205  
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
                         210                      215                      220  
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
225                      230                      235                      240  
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
                         245                      250                      255  
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
                         260                      265                      270  
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
                         275                      280                      285  
Gly Leu Lys Thr Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
                         290                      295                      300  
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
305                      310                      315                      320  
Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val

340

345

350

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Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro

355

360

365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu

370

375

380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys

385

390

395

400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys

405

410

415

&lt;210&gt; 4

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Leu Gln Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu

1

5

10

15

Pro Val Asn Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val

20

25

30

Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu

35

40

45

Phe Leu Ile Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu

50

55

60

Asn Ala Thr Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys

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85	90	95	
Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg			
100	105	110	
Gln Val Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser			
115	120	125	
Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu			
130	135	140	
Ile Ala Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe			
145	150	155	160
Tyr Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile			
165	170	175	
Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser			
180	185	190	
Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu			
195	200	205	
Gln Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp			
210	215	220	
Phe Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp			
225	230	235	240
Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly			
245	250	255	
Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe			
275	280	285	



10 /307

Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe

290

295

300

Phe Asn Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala

305

310

315

320

Tyr Leu Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val

325

330

335

Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu

340

345

350

Glu Ala Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly

355

360

365

His Pro Ile Leu Asn Asn Asn His Arg Lys Asn Asp

370

375

380

&lt;210&gt; 5

&lt;211&gt; 585

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys Trp Val Phe

1

5

10

15

Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala Ile Val Leu

20

25

30

Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln Ile Ser Arg

11 /307

50	55	60	
Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn Ser Lys Lys			
65	70	75	80
Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu Glu Ala Asp			
85	90	95	
Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly Val Pro Ile			
100	105	110	
Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu Glu Gln Trp			
115	120	125	
Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys Leu Asp Phe			
130	135	140	
Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu Arg Gln Leu			
145	150	155	160
Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn Ala Asp Ile			
165	170	175	
Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn Ala Thr Gln			
180	185	190	
Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr Leu Ser Pro			
195	200	205	
Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg Thr Tyr Thr			
210	215	220	
Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly Val Pro Gln			

245

250

255

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His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser Leu Thr Leu

260

265

270

Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu Leu Tyr Val

275

280

285

Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile Phe Glu Pro

290

295

300

Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr Arg Lys Pro

305

310

315

320

Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln Leu Pro Gly

325

330

335

Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val Gln Gly Ser

340

345

350

Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly Met Ile Leu

355

360

365

Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro Ile

370

375

380

Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu Gln

385

390

395

400

Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile Ala

405

410

415

Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu Ser

420

425

430

His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu Leu

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450                      455                      460  
 Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly Trp  
 465                      470                      475                      480  
 Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr Asp  
                     485                      490                      495  
 Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln Met  
                     500                      505                      510  
 Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg Leu  
                     515                      520                      525  
 Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro Ala  
                     530                      535                      540  
 Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg Ala  
 545                      550                      555                      560  
 Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His Lys  
                     565                      570                      575  
 Asp Leu Leu Ala His Val Gly Arg Asn  
                     580                      585

&lt;210&gt; 6

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

14 /307

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys  
20 25 30  
Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
35 40 45  
Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
50 55 60  
Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn  
65 70 75 80  
Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val  
85 90 95  
Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His  
100 105 110  
Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp  
115 120 125  
Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg  
130 135 140  
Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala  
145 150 155 160  
Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys  
165 170 175  
Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu  
180 185 190  
Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

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210	215	220	
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg			
225	230	235	240
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu			
	245	250	255
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser			
	260	265	270
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys			
	275	280	285
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe			
	290	295	300
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr			
305	310	315	320
Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
	325	330	

&lt;210&gt; 7

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile Ser Ile

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Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys Gly Pro

35

40

45

His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala Leu Ile

50

55

60

Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp Thr Phe

65

70

75

80

Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu Pro Thr

85

90

95

Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu Lys Leu

100

105

110

Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln Arg Lys

115

120

125

Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu Leu Pro

130

135

140

Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys Tyr Val

145

150

155

160

Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu Asp Trp

165

170

175

Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro Leu Leu

180

185

190

Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu Leu Ser

195

200

205

Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe Phe Ala

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225                      230                      235                      240  
 Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys Gly Cys  
                          245                      250                      255  
 Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala Arg Ala  
                          260                      265                      270  
 Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro Glu Lys  
                          275                      280                      285  
 Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile Asp Cys  
                          290                      295                      300  
 Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg Tyr Trp  
 305                      310                      315                      320  
 Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys Ser Ala  
                          325                      330                      335  
 Pro Ala Arg Ser Tyr Val Leu Arg Leu  
                          340                      345

&lt;210&gt; 8

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly

The amino acid sequence of the protein encoded by the nucleotide sequence of the
 cDNA of the present invention is identical to the amino acid sequence of the
 protein encoded by the nucleotide sequence of the cDNA of the present invention.



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Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp

35

40

45

Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys

50

55

60

Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe

65

70

75

80

Ala Asp Ile Ser Ile Leu Ser Asp Phe

85

&lt;210&gt; 9

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

1

5

10

15

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

20

25

30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

35

40

45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

50

55

60

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

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	85	90	95												
Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro	Asp	Gly	Gly	Leu	Met	Val	Leu	Pro
	100				105									110	
Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser	Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu
	115					120								125	
Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser	Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly
	130					135								140	
Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu	Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile
145						150						155			160
Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr	Leu	Ser	Ala	Thr	Phe	Gln	Gly	His
						165								170	175
Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe
						180								185	190
Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg
						195								200	205
Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly
						210								215	220
Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr
225						230								235	240
Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	Ser	Met	Gln	Glu	Gln	His	Ser	Ile
						245								250	255
Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp

275

280

285

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Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro

290

295

300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg

305

310

315

320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe

325

330

335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp

340

345

350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro

355

360

365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met

370

375

380

Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser

385

390

395

400

Glu Tyr Gln Ser Ile Asn

405

&lt;210&gt; 10

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Pro Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr

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	20		25		30										
Cys	Val	Ala	Leu	Ala	Val	Val	Leu	Ser	Ser	Val	Ser	Ile	Cys	Asp	Gly
	35						40							45	
His	Trp	Leu	Leu	Ala	Glu	Asp	Arg	Leu	Phe	Gly	Leu	Trp	His	Phe	Cys
	50						55							60	
Thr	Thr	Thr	Asn	Gln	Ser	Val	Pro	Ile	Cys	Phe	Arg	Asp	Leu	Gly	Gln
	65						70							75	
Ala	His	Val	Pro	Gly	Leu	Ala	Val	Gly	Met	Gly	Leu	Val	Arg	Ser	Val
							85							90	
Gly	Ala	Leu	Ala	Val	Val	Ala	Ala	Ile	Phe	Gly	Leu	Glu	Phe	Leu	Met
							100							105	
Val	Ser	Gln	Leu	Cys	Glu	Asp	Lys	His	Ser	Gln	Cys	Lys	Trp	Val	Met
							115							120	
Gly	Ser	Ile	Leu	Leu	Leu	Val	Ser	Phe	Val	Leu	Ser	Ser	Gly	Gly	Leu
							130							135	
Leu	Gly	Phe	Val	Ile	Leu	Leu	Arg	Asn	Gln	Val	Thr	Leu	Ile	Gly	Phe
							145							150	
Thr	Leu	Met	Phe	Trp	Cys	Glu	Phe	Thr	Ala	Ser	Phe	Leu	Leu	Phe	Leu
							155							160	
							165							170	
Asn	Ala	Ile	Ser	Gly	Leu	His	Ile	Asn	Ser	Ile	Thr	His	Pro	Trp	Glu
							175							180	
							185							190	

&lt;212&gt; DNA

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&lt;213&gt; Homo sapiens

&lt;400&gt; 11

atggtgaaga ttagcttcca gcccgccgtg gctggcatca agggcgacaa ggctgacaag 60  
 gcgtcggcgt cgccccctgc gccggcctcg gccaccgaga tctgtctgac gccggctagg 120  
 gaggagcagc ccccaacaac tcgatccaag agggggagct cagtgggcgg cgtgtgctac 180  
 ctgtcgatgg gcatggctgt gctgtcatg ggccctgtgt tcgcctctgt ctacatctac 240  
 agatacttct ttcttgcaca gctggccga gataacttct tccgtgtgg tgtgtgtat 300  
 gaggactccc tgctctccca ggtccggact cagatggagc tggaagagga tgtgaaaatc 360  
 tacctcgacg agaactacga gcgcatcaac gtgcctgtgc ccagtttg cgcggtgac 420  
 cctgcagaca tcatcatga ctccagcgg ggtctgactg cgtaccatga tatctccctg 480  
 gacaagtgt atgtcatga actcaacacc accattgtgc tgccccctcg caacttctgg 540  
 gagctcctca tgaacgtgaa gagggggacc tacctgccgc agacgtacat catccaggag 600  
 gagatgggtg tcacggagca tgtcagtac aaggaggccc tggggtcctt catctaccac 660  
 ctgtgcaacg ggaaagacac ctaccggctc cggcgcggg caacgcggag gcggatcaac 720  
 aagcgtgggg ccaagaactg caatgccatc cgccacttcg agaacacctt cgtggtggag 780  
 acgtcatct gcggggtggt g 801

&lt;210&gt; 12

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

gtgacggtgc aggagccccg ccgcggcgcc ccgtcacgt ttgcacga ccgcgggcgc 180

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tacgggcttg actcccccaa ggccgaggtc cgcggccagg tgctggcgcc gctgcccctc 240  
 cacggagttg ctgatcatct gggctgtgat ccacaaacce ggttctttgt ccttcctaat 300  
 atcaaacagt ggattgcctt gctgcagagg ggaaactgca cgtttaaaga gaaaatatca 360  
 cgggccgctt tccacaatgc agttgctgta gtcacttaca ataataaatc caaagaggag 420  
 ccagttacca tgactcatcc aggcactgga gatattattg ctgtcatgat aacagaattg 480  
 aggggtaagg atattttgag ttatctggag aaaaacatct ctgtacaaat gacaatagct 540  
 gttggaactc gaatgccacc gaagaacttc agccgtggct ctctagtctt cgtgtcaata 600  
 tcttttattg ttttgatgat tattttctca gcatggctca tattctactt cattcagaag 660  
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 gccatcagta aattgacaac caggacagta aagaagggtg acaaggaaac tgaccagac 780  
 tttgatcatt gtgcagtctg catagagagc tataagcaga atgatgtcgt ccgaattctc 840  
 cctgcaagc atgttttcca caaatcctgc gtggatccct ggcttagtga acattgtacc 900  
 tgtcctatgt gcaaacttaa tatattgaag gccctgggaa ttgtgccgaa ttgccatgt 960  
 actgataacg tagcattcga tatggaaagg ctcaccagaa cccaagctgt taaccgaaga 1020  
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 gcagtaacaa aagaatggtt tattattgcc agttttggcc tcctcagtgc cctcacactc 1200  
 tgctacatga tcacagagc cacagctagc ttgaatgcta atgaggtaga atggttt 1257

&lt;210&gt; 13

&lt;211&gt; 1245

&lt;212&gt; DNA

(b) (1)

atgaggggcg cgaacgcctg ggcgccactc tgcttgetgc tggetgccgc caccagctc 60

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tcgcggcagc agtccccaga gagacctgtt ttcacatgtg gtggcattct tactggagag 120  
tctggattta ttggcagtga aggttttctt ggagtgtagc ctccaaatag caaatgtact 180  
tggaatatca cagttccga aggaaaagta gtcgttctca atttccgatt catagacctc 240  
gagagtgaca acctgtgccg ctatgacttt gtggatgtgt acaatggcca tgccaatggc 300  
cagcgcattg gccgtttctg ttggcacttt cgccctggag cccttgtgtc cagtggcaac 360  
aagatgatgg tgcagatgat ttctgatgcc aacacagctg gcaatggctt catggccatg 420  
ttctccgctg ctgaacaaaa cgaaagaggg gatcagtatt gtggaggact ccttgacaga 480  
ccttccggtt cttttaaaac ccccaactgg ccagaccggg attacctgc aggagtcaat 540  
tgtgtgtggc acattgtagc cccaaagaat cagcttatag aattaaagt tgagaagttt 600  
gatgtggagc gagataacta ctgccgatat gattatgtgg ctgtgtttaa tggcggggaa 660  
gtcaacgatg ctagaagaat tggaagtat tgtggtgata gtccacctgc gccaatgtg 720  
tctgagagaa atgaacttct tattcagttt ttatcagact taagttaaac tgcagatggg 780  
tttattggtc actacatatt caggccaaaa aaactgccta caactacaga acagcctgtc 840  
accaccacat tccctgtaac caggggttta aaaaccaccg tggccttgtg tcaacaaaag 900  
tgtagacgga cggggactct ggagggcaat tattgttcaa gtgactttgt attagccggc 960  
actgttatca caaccatcac tcgcgatggg agtttgcacg ccacagtctc gatcatcaac 1020  
atctacaaag agggaaattt ggcgattcag caggcgggca agaacatgag tgccaggctg 1080  
actgtcgtct gcaagcagtg cctctcctc agaagaggtc taaattacat tattatgggc 1140  
caagtaggtg aagatgggag aggcataatc atgccaaaca gctttatcat gatgttcaag 1200  
accaagaatc agaagctcct ggatgcctta aaaaataagc aatgt 1245

&lt;210&gt; 14

cDNA

&lt;213&gt; Homo sapiens

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&lt;400&gt; 14

atgctccaga ccttgtatga ttacttctgg tgggaacgtc tgtggctgcc tgtgaacttg	60
acctgggccc atctagaaga ccgagatgga cgtgtctacg ccaaagcctc agatctctat	120
atcacgtgc cccitggcctt gctcttccctc atcgttcgat acttctttga gctgtacgtg	180
gctacaccac tggttgcctt cttgaacata aaggagaaaa ctgggtgcg ggcacctccc	240
aacgccacct tggaacattt ctacctgacc agtggcaagc agcccaagca ggtggaagta	300
gagcttttgt cccggcagag cgggctctct ggccgccagg tagagcgttg gttccgtcgc	360
cgccgcaacc aggaccggcc cagtctctc aagaagttcc gagaagccag ctggagattc	420
acattttacc tgattgcctt cattgccggc atggccgtca ttgtggataa accctgggtc	480
tatgacatga agaaagtttg ggagggatat cccatacaga gcactatccc ttcccagtat	540
tggtactaca tgattgaact ttcttctac tggtcctgc tcttcagcat tgcctctgat	600
gtcaagcgaa aggatttcaa ggaacagatc atccaccatg tgccaccat cattctcctc	660
agcttttctt ggtttgccaa ttacatccga gctgggactc taatcatggc tctgcatgac	720
tcttccgatt acctgctgga gtcagccaag atgtttaact acgcgggatg gaagaacacc	780
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tacctcattt tgcgcatggc ccacaagttc ataactggaa agctggtaga agatgaacgc	1020
agtgaccggg aagaaacaga gagctcagag ggggaggagg ctgcagctgg gggaggagca	1080
aagagccggc cctagccaa tggccacccc atcctcaata acaaccatcg taagaatgac	1140

&lt;210&gt; 15

GAGGAGGAGG

&lt;213&gt; Homo sapiens



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&lt;400&gt; 15

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tgtgagctgg aggcctgcag cctgatgcc gacatgctgg actacctgct gaggctgggc	180
cagatcagcc ggcgagatgc cttggaggtc acctggtacc acgcagccaa cagcaagaaa	240
gccatgacag ctgccctgaa cagcaacatc acagtccctgg aggtgacgt caatgtagaa	300
gggctcggca cagccaatga gacaggagtt cccatcatgg cacaccccc cactatctac	360
agtgacaaca cactggagca gtggctggac gctgtgctgg gctcttccca aaagggcac	420
aaactggact tcaagaacat caaggcagtg ggccccctcc tggacctct gcggcagctg	480
acagaggaag gcaaagtccg gcggcccata tggatcaacg ctgacatctt aaagggcccc	540
aacatgctca tctcaactga ggtcaatgcc acacagttcc tggccctggt ccaggagaag	600
tatcccaagg ctacctatc tccaggttg accaccttct acatgtccac gtcccaaac	660
aggacgtaca cccaagccat ggtggagaag atgcacgagc tgggtggagg agtgccccag	720
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ctgctgagcc aatctgagag gtacagcctg acgtgtggc aggtgcctc ggaccccatg	840
tcggtggaag atctgtctc cgtccgggat aacactgctg tccaccaagt ctactatgac	900
atctttgagc ctctcctgtc acagttcaag cagctggcct tgaatgccac acggaaacca	960
atgtactaca caggaggcag cctgatccct cttctccagc tgcctgggga tgacggtctg	1020
aatgtggagt ggctggttcc tgacgtccag ggcagcggta aaacagcaac aatgacctc	1080
ccagacacag aaggcatgat cctgctgaac actggcctcg agggaactgt ggtgaaaac	1140
cccggtccca ttgttcatac tccaagtggc aacatcctga cgtggagtc ctgctgcag	1200
cagctggcca cacatcccg acactggggc atccatttgc aaatagcgga gcccgagcc	1260
agagagctgc ttacagctgt ggtgaggtc tcccccaag tgactgtggc accaggttg	1440

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cctgaggagg tgctgggcag tggctacagg gaacagctgc tcacagatat gctagagttg 1500  
 tgccaggggc tctggcaacc tgtgtccttc cagatgcagg ccatgctgct gggccacagc 1560  
 acagctggag ccataggcag gctgctggca tctctcccc gggccaccgt cacagtggag 1620  
 cacaaccag ctgggggcga ctatgcctct gtgaggacag cattgctggc agctagggt 1680  
 gtggacagga cccgagtcta ctacaggcta cccagggt accacaagga cttgctggct 1740  
 catgttggt gaaac 1755

&lt;210&gt; 16

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

atgtggctgt gggaggacca gggcggcctc ctgggccctt tctccttct gctgctagt 60  
 ctgctgctgg tgacgcggag cccggtcaat gctgcctcc tcaccggcag cctcttcgtt 120  
 ctactgcgcg tcttcagctt tgagccggtg cctcttgca gggccctgca ggtgctcaag 180  
 ccccgggacc gcatttctgc catgcccac cgtggcggca gccacgacgc gcccgagaac 240  
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 gagtttactt ctgacgggat tctgtctta atgcacgata acacagtaga taggacgact 360  
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 gcaaaccaca gactcaggaa tgatttccct gatgaaaaga tcctaccct aagggaagct 480  
 gttgcagagt gcctaaacca taacctcaca atcttctttg atgtcaaagg ccatgcacac 540  
 aaggctactg aggtctctaaa gaaaatgtat atggaatttc ctcaactgta taataatagt 600  
 tatgatactt tctggaacaa ttttatattt gttatgatgg acattttgct cgattggagc 780

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atgcataata tcttgttgga cctgtgtgga atttcagctt tctcatgca aaaggatttt 840  
 gtatccccgg cctacttgaa gaagtggta gctaaaggaa tccaggttgt tggttggact 900  
 gttaatacct ttgatgaaaa gagttactac gaatcccatc ttggttccag ctatatacct 960  
 gacagcatgg tagaagactg cgaacctcac ttc 993

&lt;210&gt; 17

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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 ctacccctgt tcacctgtgg cccccacact ttgcattctc tggtcacat cctcgggacc 180  
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 gacctgcac tggcccagag gaaggaaatg gcctcaggct tcagcaaggg gccaccctg 420  
 gggctgctgc ccgacgtgcc ctccctgatg gagacactca gctacagcta ctgctacgtg 480  
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 ttcgccctgc tgttctgct ctctctcac ctcttcccgc tggaggccgt gcgcgaggac 660  
 gccttctacg ccgcgccgt gccgcgccgc ctcttctaca tgatccccgt cttcttcgcc 720

ccacccccca gcagtcgga gaaggcggt tcttggagt atgactatga gaccatccgc 900

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aacatcgact gctacagcac agatttctgc gtgcgggtgc gcgatggcat gcggtactgg 960  
aacatgacgg tgcagtgggtg gctggcgcag tatatctaca agagcgcacc tgcccgttcc 1020  
tatgtcctgc gcctt 1035

<210> 18

&lt;211&gt; 267

&lt;212&gt; DNA

<213> Homo sapiens

&lt;400&gt; 18

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ggcgtcctct tctcgccgt ctccatcgt gccttctgca cttcctcgt gctggccatc	120
acccggcac agagcctcac agaccccacc agctactacc tctccagcgt ctggagcttc	180
atttccttca agtgggcctt cctgctcagc ctctatgcc accgctaccg ggtgacttt	240
gctgacatca gcatactcag cgatttc	267

&lt;210&gt; 19

<211> 1218

&lt;212&gt; DNA

<213> Homo sapiens

&lt;400&gt; 19

atgcgcggct ctgtggagtg cacctggggt tgggggcact gtgccccag cccctgctc 60  
ctttggactc tactttctgtt tgcagcccca tttggcctgc tgggggagaa gaccgccag 120

DECLASSIFIED BY: 6032 GPO ON 08-09-2013

gtaatggtgg ccaccaacac cccccacagc accctgagcg tcaactggag cctcctgcta 300

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tccctgagc ccgatggggg cctgatggtg ctcctaagg acagcattca gttttcttct 360  
 gcccttggtt ttaccagget gcttgagttt gacagacca acgtgtccga tacggcagca 420  
 aagcctttgg gaagaccata tctccatac tcttggcg atttctcttg gaacaacatc 480  
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 cctaccagga cttttgcaa tggcagcctg gccttcaggg tccaggcctt tccagggtcc 600  
 agccgaccag cccaaccccc tgcctcctg cacacagcag acacctgtca gctagagggtg 660  
 gccctgattg gacccctcc cgggggaaac cgttcctgt ttgggctgga ggtagccaca 720  
 ttgggccagg gccctgactg cccctcaatg caggagcagc actccatga cgatgaatat 780  
 gcaccggcgg tcttcagtt ggaccageta ctgtggggct cctcccatc aggttttga 840  
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 gccttctttg ggtcccagaa taacttctgt gccttcaatc tgacgttcgg ggttccaca 1020  
 ggccctggct attgggacca acactacctc agctggctga tgctcctggg tgtgggcttc 1080  
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 gattaccagt ccataaat 1218

&lt;210&gt; 20

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

tctcggtct ccatttga tgggcactgg ctcctggtg aggaccgct cttegggtc 180

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tggcacttct gcaccaccac caaccagagt gtgccgatct gcttcagaga cctggggccag 240  
 gcccattgtgc cegggctggc cgtgggcatg ggccctggtac gcagcgtggg cgccttggcc 300  
 gtgggtggccg ccatttttgg cctggagttc ctcatggtgt cccagttgtg cgaggacaaa 360  
 cactcacagt gcaagtgggt catgggttcc atctctctcc tgggtgtcttt cgtctctctcc 420  
 tccggcgggc tectgggttt tgtgatctc ctcaggaacc aagtcacact catcggttc 480  
 accctaagt tttggtgga attcaactgcc tcttctctcc tcttctgaa cgccatcagc 540  
 ggcttcaca tcaacagcat caccatccc tgggaa 576

&lt;210&gt; 21

&lt;211&gt; 2042

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (91)... (894)

&lt;400&gt; 21

tccggtgcct gcagagctcg gagcggcgga ggcagagacc gaggtgcac cggcagaggc 60  
 tgcggggcgg acgcgcgggc cggcgcagcc atg gtg aag att agc ttc cag 111

Met Val Lys Ile Ser Phe Gln

1

5

ccc gcc gtg gct ggc atc aag ggc gac aag gct gac aag gcg tcg gcg 159  
 Pro Ala Val Ala Gly Ile Lys Gly Asp Lys Ala Asp Lys Ala Ser Ala

Ser Ala Pro Ala Pro Ala Ser Ala Thr Glu Ile Leu Leu Thr Pro Ala

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25	30	35	
agg gag gag cag ccc cca caa cat cga tcc aag agg ggg agc tca gtg			255
Arg Glu Glu Gln Pro Pro Gln His Arg Ser Lys Arg Gly Ser Ser Val			
40	45	50	55
ggc ggc gtg tgc tac ctg tgc atg ggc atg gtc gtg ctg ctc atg ggc			303
Gly Gly Val Cys Tyr Leu Ser Met Gly Met Val Val Leu Leu Met Gly			
60	65	70	
ctc gtg ttc gcc tct gtc tac atc tac aga tac ttc ttt ctt gca cag			351
Leu Val Phe Ala Ser Val Tyr Ile Tyr Arg Tyr Phe Phe Leu Ala Gln			
75	80	85	
ctg gcc cga gat aac ttc ttc cgc tgt ggt gtg ctg tat gag gac tcc			399
Leu Ala Arg Asp Asn Phe Phe Arg Cys Gly Val Leu Tyr Glu Asp Ser			
90	95	100	
ctg tcc tcc cag gtc cgg act cag atg gag ctg gaa gag gat gtg aaa			447
Leu Ser Ser Gln Val Arg Thr Gln Met Glu Leu Glu Glu Asp Val Lys			
105	110	115	
atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc cag			495
Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro Gln			
120	125	130	135
ttt ggc ggc ggt gac cct gca gac atc atc cat gac ttc cag cgg ggt			543
Phe Gly Gly Gly Asp Pro Ala Asp Ile Ile His Asp Phe Gln Arg Gly			
140	145	150	
155	160	165	

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ctc aac acc acc att gtg ctg ccc cct cgc aac ttc tgg gag ctc ctc 639  
 Leu Asn Thr Thr Ile Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu  
 170 175 180  
 atg aac gtg aag agg ggg acc tac ctg ccg cag acg tac atc atc cag 687  
 Met Asn Val Lys Arg Gly Thr Tyr Leu Pro Gln Thr Tyr Ile Ile Gln  
 185 190 195  
 gag gag atg gtg gtc acg gag cat gtc agt gac aag gag gcc ctg ggg 735  
 Glu Glu Met Val Val Thr Glu His Val Ser Asp Lys Glu Ala Leu Gly  
 200 205 210 215  
 tcc ttc atc tac cac ctg tgc aac ggg aaa gac acc tac cgg ctc cgg 783  
 Ser Phe Ile Tyr His Leu Cys Asn Gly Lys Asp Thr Tyr Arg Leu Arg  
 220 225 230  
 cgc cgg gca acg cgg agg cgg atc aac aag cgt ggg gcc aag aac tgc 831  
 Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys Arg Gly Ala Lys Asn Cys  
 235 240 245  
 aat gcc atc cgc cac ttc gag aac acc ttc gtg gtg gag acg ctc atc 879  
 Asn Ala Ile Arg His Phe Glu Asn Thr Phe Val Val Glu Thr Leu Ile  
 250 255 260  
 tgc ggg gtg gtg tgaggectc cteccccaga accccctgcc gtgtctc 930  
 Cys Gly Val Val  
 265  
 tttttttttt tccggtgct ctctggccct cctcttccc cctgcttagc ttgtacttg 990  
 gtagagaggaga tgctgcaaag tgttttctgt gtccactgt cttgaagctg ggccctgcaa 1170



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agcctggggcc cacagctgca cgggcagccc aaggggaagg accggttggg ggagccgggc 1230  
atgtgaggcc ctgggcaagg ggatggggct gtgggggcgg ggcggcatgg gcttcagaag 1290  
tatctgcaca attagaaaag tcttcagaag ctttttcttg gaggtacac tttcttact 1350  
gtccctattc ctagacctgg ggcttgagct gaggatggga cgatgtgcc aggagaggac 1410  
ccaccagagc acaagagaag gtggctacct gggggtgtcc cagggaactct gtcagtgcct 1470  
tcagcccacc agcaggagct tggagtttgg ggagtgggga tgagtccgtc aagcacaact 1530  
gttctctgag tggaaccaa gaagcaagga gctaggacct ccagtcctgc cccccaggag 1590  
cacaagcagg gtccctcag tcaaggcagt gggatgggcg gctgaggaac ggggcaggca 1650  
aggtcactgc tcagtcactg ccacggggga cgagccgtgg gttctgctga gtaggtggag 1710  
ctcattgctt tctccaagct tggaactgtt ttgaaagata acacagagg aaaggagag 1770  
ccacctggta cttgtccacc ctgcctctc tgttctgaaa ttccatcccc ctcagcttag 1830  
gggaatgcac cttttccct ttccttctca cttttgcatg tttttactga tcattcgata 1890  
tgctaaccgt tctcagccct gagccttgga gaggagggt gtaacgcctt cagtcagtct 1950  
ctggggatga aactctaaa tgctttgtat attttctcaa ttagatctct tttcagaagt 2010  
gtctatagaa caataaaaat cttttacttc tg 2042

&lt;210&gt; 22

&lt;211&gt; 1433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)... (1264)

Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala

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1	5	10	
ctc gcc ctg ctg acc tgc agc ctg tgg ccg gca cgg gca gac aac gcg			94
Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala			
15	20	25	30
agc cag gag tac tac acg gcg ctc atc aac gtg acg gtg cag gag ccc			142
Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro			
35	40	45	
ggc cgc ggc gcc ccg ctc acg ttt cgc atc gac cgc ggg cgc tac ggg			190
Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly			
50	55	60	
ctt gac tcc ccc aag gcc gag gtc cgc ggc cag gtg ctg gcg ccg ctg			238
Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu			
65	70	75	
ccc ctc cac gga gtt gct gat cat ctg ggc tgt gat cca caa acc cgg			286
Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg			
80	85	90	
ttc ttt gtc cct cct aat atc aaa cag tgg att gcc ttg ctg cag agg			334
Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg			
95	100	105	110
gga aac tgc acg ttt aaa gag aaa ata tca cgg gcc gct ttc cac aat			382
Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn			
115	120	125	
130	135	140	

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acc atg act cat cca ggc act gga gat att att gct gtc atg ata aca	478
Thr Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr	
145 150 155	
gaa ttg agg ggt aag gat att ttg agt tat ctg gag aaa aac atc tct	526
Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser	
160 165 170	
gta caa atg aca ata gct gtt gga act cga atg cca ccg aag aac ttc	574
Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe	
175 180 185 190	
agc cgt ggc tct cta gtc ttc gtg tca ata tcc ttt att gtt ttg atg	622
Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met	
195 200 205	
att att tct tca gca tgg ctc ata ttc tac ttc att cag aag atc agg	670
Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg	
210 215 220	
tac aca aat gca cgc gac agg aac cag cgt cgt ctc gga gat gca gcc	718
Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala	
225 230 235	
aag aaa gcc atc agt aaa ttg aca acc agg aca gta aag aag ggt gac	766
Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp	
240 245 250	
aag gaa act gac cca gac ttt gat cat tgt gca gtc tgc ata gag agc	814
tat aag cag aat gat gtc gtc cga att ctc ccc tgc aag cat gtt ttc	862

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Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe  
 275 280 285  
 cac aaa tcc tgc gtg gat ccc tgg ctt agt gaa cat tgt acc tgt cct 910  
 His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro  
 290 295 300  
 atg tgc aaa ctt aat ata ttg aag gcc ctg gga att gtg ccg aat ttg 958  
 Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu  
 305 310 315  
 cca tgt act gat aac gta gca ttc gat atg gaa agg ctc acc aga acc 1006  
 Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr  
 320 325 330  
 caa gct gtt aac cga aga tca gcc ctc ggc gac ctc gcc ggc gac aac 1054  
 Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn  
 335 340 345 350  
 tcc ctt ggc ctt gag cca ctt cga act tcg ggg atc tca cct ctt cct 1102  
 Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro  
 355 360 365  
 cag gat ggg gag ctc act ccg aga aca gga gaa atc aac att gca gta 1150  
 Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val  
 370 375 380  
 aca aaa gaa tgg ttt att att gcc agt ttt ggc ctc ctc agt gcc ctc 1198  
 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu  
 385 390 395  
 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn

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400	405	410	
gag gta gaa tgg ttt tgaagaagaa aaaacctgct ttctgactga ttttgcctt			1300
Glu Val Glu Trp Phe			
415			
gaaggaaaaa agaacctatt tttgtgcatc atttaccaat catgccacac aagcatttat			1360
ttttagtaca ttttattttt tcataaaatt gctaatagcca aagctttgta ttaaaagaaa			1420
taaataataa aat			1433

<210> 23

&lt;211&gt; 1917

## <212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

 $\langle 222 \rangle$  (210)... (1457)

&lt;400&gt; 23

gtatcccccg gctacctggg ccgccccgcg gcggtgcgcg cgtgagaggg agcgcgcggg 60  
cagccgagcg ccggtgtgag ccagcgctgc tgccagtgtg agccagcgct gctgccagtg 120  
tgagcggcgg tgtgagcgcg gtgggtgcgg aggggcgtgt gtgccggcgc gcgcgccgtg 180  
gggtgcaaac cccgagcgtc tacgtgcc atg agg ggc gcg aac gcc tgg gcg 233

Met Arg Gly Ala Asn Ala Trp Ala

1

5

10

15

20



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Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe Lys Thr Pro  
 155 160 165  
 aac tgg cca gac cgg gat tac cct gca gga gtc act tgt gtg tgg cac 761  
 Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr Cys Val Trp His  
 170 175 180  
 att gta gcc cca aag aat cag ctt ata gaa tta aag ttt gag aag ttt 809  
 Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu Lys Phe Glu Lys Phe  
 185 190 195 200  
 gat gtg gag cga gat aac tac tgc cga tat gat tat gtg gct gtg ttt 857  
 Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr Asp Tyr Val Ala Val Phe  
 205 210 215  
 aat ggc ggg gaa gtc aac gat gct aga aga att gga aag tat tgt ggt 905  
 Asn Gly Gly Glu Val Asn Asp Ala Arg Arg Ile Gly Lys Tyr Cys Gly  
 220 225 230  
 gat agt cca cct gcg cca att gtg tct gag aga aat gaa ctt ctt att 953  
 Asp Ser Pro Pro Ala Pro Ile Val Ser Glu Arg Asn Glu Leu Leu Ile  
 235 240 245  
 cag ttt tta tca gac tta agt tta act gca gat ggg ttt att ggt cac 1001  
 Gln Phe Leu Ser Asp Leu Ser Leu Thr Ala Asp Gly Phe Ile Gly His  
 250 255 260  
 tac ata ttc agg cca aaa aaa ctg cct aca act aca gaa cag cct gtc 1049  
 Tyr Ile Phe Arg Pro Lys Lys Leu Pro Thr Thr Thr Glu Gln Pro Val  
 265 270 275 280 285 290 295 300  
 Thr Thr Thr Phe Pro Val Thr Thr Gly Leu Lys Thr Thr Val Ala Leu

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285	290	295	
tgt caa caa aag tgt aga cgg acg ggg act ctg gag ggc aat tat tgt			1145
Cys Gln Gln Lys Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys			
300	305	310	
tca agt gac ttt gta tta gcc ggc act gtt atc aca acc atc act cgc			1193
Ser Ser Asp Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg			
315	320	325	
gat ggg agt ttg cac gcc aca gtc tgc atc atc aac atc tac aaa gag			1241
Asp Gly Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu			
330	335	340	
gga aat ttg gcg att cag cag gcg ggc aag aac atg agt gcc agg ctg			1289
Gly Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu			
345	350	355	360
act gtc gtc tgc aag cag tgc cct ctc ctc aga aga ggt cta aat tac			1337
Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn Tyr			
365	370	375	
att att atg ggc caa gta ggt gaa gat ggg cga ggc aaa atc atg cca			1385
Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile Met Pro			
380	385	390	
aac agc ttt atc atg atg ttc aag acc aag aat cag aag ctc ctg gat			1433
Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys Leu Leu Asp			
395	400	405	
410	415		



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tgtattctgc cattgccttt gaaagatcta tggtctctca gtagaaaaaa aaatacttat 1540  
 aaaattacat attctgaaag aggattccga aagatgggac tggttgactc ttcacatgat 1600  
 ggaggtatga ggcctccgag atagctgagg gaagttcttt gcctgctgtc agaggagcag 1660  
 ctatctgatt ggaaacctgc cgacttagtg cggatgatagg aagctaaaag tgtcaagcgt 1720  
 tgacagcttg gaagcgttta ttataacatc tctgtaaaag gatatttttag aattgagttg 1780  
 tgtgaagatg tcaaaaaaag attttagaag tgcaatattt atagtgttat ttgtttcacc 1840  
 ttcaagcctt tgccctgagg tgttacaatc ttgtcttgcg ttttctaaat caatgcttaa 1900  
 taaaatattt ttaaagg 1917

&lt;210&gt; 24

&lt;211&gt; 2258

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (225)... (1367)

&lt;400&gt; 24

tttttccgg ctgggctcgg gtcagctcg actgggctcg gcgggcggcg gcggcggcgc 60  
 ccgcggctgg cggaggaggg agggcgaggg cgggcgcggg ccggcgggcg ggcggaagag 120  
 ggaggagagg cgcggggagc caggcctcgg ggcctcggag caaccacccg agcagacgga 180  
 gtacacggag cagcggcccc ggccccgcc aagctgccgc cggg atg etc cag 233

Met Leu Gln

Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu Pro Val Asn

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5	10	15	
ttg acc tgg gcc gat cta gaa gac cga gat gga cgt gtc tac gcc aaa			329
Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val Tyr Ala Lys			
20	25	30	35
gcc tca gat ctc tat atc acg ctg ccc ctg gcc ttg ctc ttc ctc atc			377
Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu Phe Leu Ile			
40	45	50	
gtt cga tac ttc ttt gag ctg tac gtg gct aca cca ctg gct gcc ctc			425
Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu Ala Ala Leu			
55	60	65	
ttg aac ata aag gag aaa act cgg ctg cgg gca cct ccc aac gcc acc			473
Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro Asn Ala Thr			
70	75	80	
ttg gaa cat ttc tac ctg acc agt ggc aag cag ccc aag cag gtg gaa			521
Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys Gln Val Glu			
85	90	95	
gta gag ctt ttg tcc cgg cag agc ggg ctc tct ggc cgc cag gta gag			569
Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg Gln Val Glu			
100	105	110	115
cgt tgg ttc cgt cgc cgc cgc aac cag gac cgg ccc agt ctc ctc aag			617
Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser Leu Leu Lys			
120	125	130	
135	140	145	

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att gcc ggc atg gcc gtc att gtg gat aaa ccc tgg ttc tat gac atg	713
Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met	
150 155 160	
aag aaa gtt tgg gag gga tat ccc ata cag agc act atc cct tcc cag	761
Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln	
165 170 175	
tat tgg tac tac atg att gaa ctt tcc ttc tac tgg tcc ctg ctc ttc	809
Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe	
180 185 190 195	
agc att gcc tct gat gtc aag cga aag gat ttc aag gaa cag atc atc	857
Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile	
200 205 210	
cac cat gtg gcc acc atc att ctc atc agc ttt tcc tgg ttt gcc aat	905
His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn	
215 220 225	
tac atc cga gct ggg act cta atc atg gct ctg cat gac tct tcc gat	953
Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp	
230 235 240	
tac ctg ctg gag tca gcc aag atg ttt aac tac gcg gga tgg aag aac	1001
Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn	
245 250 255	
acc tgc aac aac atc ttc atc gtc ttc gcc att gtt ttt atc atc acc	1049
cga ctg gtc atc ctg ccc ttc tgg atc ctg cat tgc acc ctg gtg tac	1097

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Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val Tyr  
 280 285 290  
 cca ctg gag ctc tat cct gcc ttc ttt ggc tat tac ttc ttc aat tcc 1145  
 Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn Ser  
 295 300 305  
 atg atg gga gtt cta cag ctg ctg cat atc ttc tgg gcc tac ctc att 1193  
 Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu Ile  
 310 315 320  
 ttg cgc atg gcc cac aag ttc ata act gga aag ctg gta gaa gat gaa 1241  
 Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp Glu  
 325 330 335  
 cgc agt gac cgg gaa gaa aca gag agc tca gag ggg gag gag gct gca 1289  
 Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala Ala  
 340 345 350 355  
 gct ggg gga gga gca aag agc cgg ccc cta gcc aat ggc cac ccc atc 1337  
 Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro Ile  
 360 365 370  
 ctc aat aac aac cat cgt aag aat gac tgaaccatta ttccagctgc ctccca 1390  
 Leu Asn Asn Asn His Arg Lys Asn Asp  
 375 380  
 gattaatgca taaagccaag gaactaccct gctccctgcg ctatagggtc actttaagct 1450  
 ctggggaaaa aggagaaagt gagaggagag ttctctgcat cctccctcct tgcttgctac 1510  
 gcttttgagg cctccctca gctctctgtg ggtaggggtt acaattcaca ttcttattc 1690

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tgagaatttg gccccagctg ttgaccttg actccctgac ctccagagcc agggttgtgc 1750  
 cttattgtcc catctgtggg cctcattctg ccaaagctgg accaaggcta acctttctaa 1810  
 gctccctaac ttgggccaga aaccaaagct gagcttttaa cttctccct ctatgacaca 1870  
 aatgaattga gggtaggagg aggggtgcaca taacccttac cctacctctg ccaaaaagtg 1930  
 ggggctgtac tggggactgc tcggatgac tttcttagtg ctacttctt cagctgtccc 1990  
 tgtagcgaca ggtctaagat ctgactgcct ctttctctg gcctcttccc cttccctct 2050  
 tctcttcagc taggctagct ggtttggagt agaattggca ctaattctaa tttttattta 2110  
 ttaaataattt ggggttttgg ttttaaagcc agaattacgg ctagcaccta gcatttcagc 2170  
 agagggacca ttttagacca aaatgtactg ttaatgggtt tttttttaa attaaaagat 2230  
 taaataaaaa atattaaata aaacatgg 2258

&lt;210&gt; 25

&lt;211&gt; 1973

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (130)... (1887)

&lt;400&gt; 25

gagcagacca gggccggtgg agaattaggt gctgctggga gctcctgcct cccacaggat 60  
 tccagctgca gggagcctca gggactctgg gccgcacgga gttgggggca ttccccagag 120  
 agcgtcgcc atg gtc tgc agg gag cag tta tca aag aat cag gtc aag 168

tgg gtg ttt gcc ggc att acc tgt gtg tct gtg gtg gtc att gcc gca 216

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Trp Val Phe Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala  
 15 20 25  
 ata gtc ctt gcc atc acc ctg cgg cgg cca ggc tgt gag ctg gag gcc 264  
 Ile Val Leu Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala  
 30 35 40 45  
 tgc agc cct gat gcc gac atg ctg gac tac ctg ctg agc ctg ggc cag 312  
 Cys Ser Pro Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln  
 50 55 60  
 atc agc cgg cga gat gcc ttg gag gtc acc tgg tac cac gca gcc aac 360  
 Ile Ser Arg Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn  
 65 70 75  
 agc aag aaa gcc atg aca gct gcc ctg aac agc aac atc aca gtc ctg 408  
 Ser Lys Lys Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu  
 80 85 90  
 gag gct gac gtc aat gta gaa ggg ctc ggc aca gcc aat gag aca gga 456  
 Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly  
 95 100 105  
 gtt ccc atc atg gca cac ccc ccc act atc tac agt gac aac aca ctg 504  
 Val Pro Ile Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu  
 110 115 120 125  
 gag cag tgg ctg gac gct gtg ctg ggc tct tcc caa aag ggc atc aaa 552  
 Glu Gln Trp Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys  
 130 140  
 Leu Asp Phe Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu

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145	150	155	
cgg cag ctg aca gag gaa ggc aaa gtc cgg cgg ccc ata tgg atc aac			648
Arg Gln Leu Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn			
160	165	170	
gct gac atc tta aag ggc ccc aac atg ctc atc tca act gag gtc aat			696
Ala Asp Ile Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn			
175	180	185	
gcc aca cag ttc ctg gcc ctg gtc cag gag aag tat ccc aag gct acc			744
Ala Thr Gln Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr			
190	195	200	205
cta tct cca ggc tgg acc acc ttc tac atg tcc acg tcc cca aac agg			792
Leu Ser Pro Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg			
210	215	220	
acg tac acc caa gcc atg gtg gag aag atg cac gag ctg gtg gga gga			840
Thr Tyr Thr Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly			
225	230	235	
gtg ccc cag agg gtc acc ttc cct gta cgg tct tcc atg gtg cgg gct			888
Val Pro Gln Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala			
240	245	250	
gcc tgg ccc cac ttc agc tgg ctg ctg agc caa tct gag agg tac agc			936
Ala Trp Pro His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser			
255	260	265	
			984
270	275	280	285

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ctc tac gtc cgg gat aac act gct gtc cac caa gtc tac tat gac atc	1032
Leu Tyr Val Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile	
290 295 300	
ttt gag cct ctc ctg tca cag ttc aag cag ctg gcc ttg aat gcc aca	1080
Phe Glu Pro Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr	
305 310 315	
cgg aaa cca atg tac tac aca gga ggc agc ctg atc cct ctt ctc cag	1128
Arg Lys Pro Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln	
320 325 330	
ctg cct ggg gat gac ggt ctg aat gtg gag tgg ctg gtt cct gac gtc	1176
Leu Pro Gly Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val	
335 340 345	
cag ggc agc ggt aaa aca gca aca atg acc ctc cca gac aca gaa ggc	1224
Gln Gly Ser Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly	
350 355 360 365	
atg atc ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc	1272
Met Ile Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro	
370 375 380	
gtg ccc att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc	1320
Val Pro Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser	
385 390 395	
tgc ctg cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg	1368
caa ata ggc gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca	1416



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Gln Ile Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala  
 415 420 425  
 cgc ctc tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc 1464  
 Arg Leu Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala  
 430 435 440 445  
 aaa atc tcc cac ggg agt ttt tcg gtc ccc ggc cat gtg gct ggc aga 1512  
 Lys Ile Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg  
 450 455 460  
 gag ctg ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca 1560  
 Glu Leu Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala  
 465 470 475  
 cca ggc tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg 1608  
 Pro Gly Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu  
 480 485 490  
 ctc aca gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc 1656  
 Leu Thr Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser  
 495 500 505  
 ttc cag atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata 1704  
 Phe Gln Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile  
 510 515 520 525  
 ggc agg ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac 1752  
 Gly Arg Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His  
 Asn Pro Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala

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545	550	555	
gct agg gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc			1848
Ala Arg Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly			
560	565	570	
tac cac aag gac ttg ctg gct cat gtt ggt aga aac tgagcaccca ggggtg			1900
Tyr His Lys Asp Leu Leu Ala His Val Gly Arg Asn			
575	580	585	
gtgggccagc ggacctcagg gcggaggctt cccacgggga ggcaggaaga aataaaggtc			1960
tttgctttc tcc			1973

&lt;210&gt; 26

&lt;211&gt; 1606

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (135)... (1130)

&lt;400&gt; 26

attgtgcggc gctggteccc tcagagggtt cctgctgctg ccggtgcctt ggacctccc	60
cctcgtttct cgttctactg cccaggage ccggcgggtc cgggactccc gtccgtgcgc	120
gtgcgggcgc cggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc	170

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly

Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro

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15	20	25	
gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc			266
Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val			
30	35	40	
ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag			314
Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys			
45	50	55	60
ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac			362
Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp			
65	70	75	
gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga			410
Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly			
80	85	90	
gca aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct			458
Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro			
95	100	105	
gtc tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg			506
Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly			
110	115	120	
cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca			554
Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala			
125	130	135	140
145	150	155	

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cta agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc	650
Leu Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe	
160 165 170	
ttt gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa	698
Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys	
175 180 185	
atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct	746
Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser	
190 195 200	
ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta	794
Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val	
205 210 215 220	
ata aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat	842
Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp	
225 230 235	
ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg	890
Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met	
240 245 250	
atg gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg	938
Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu	
255 260 265	
tgt gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc	986
tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act	1034

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Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr  
 285                      290                      295                      300  
 gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc      1082  
 Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser  
                          305                      310                      315  
 agc tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc      1127  
 Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe  
                          320                      325                      330  
 tag actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatalc      1180  
 aggatatca aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca      1240  
 aatgcaatag ttggtcactg catttttacc tgaaccaaag ctaaaccgg tggtgccacc      1300  
 atgcaccatg gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa      1360  
 cgcacaagag cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag      1420  
 cacagattga attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa      1480  
 ctcagagttg acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt      1540  
 taacatgtac tgtagacatc aaacttgttg ccatactaataaaaattatta aaaggagcac      1600  
 taaagg      1606

&lt;210&gt; 27

&lt;211&gt; 2380

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;222&gt; (247)... (1284)

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&lt;400&gt; 27

agtgtggacc tggactcgaa tcccggtgcc gactcgcgct ctgggttct gtcgccgggc 60  
 ttcttcctg cccgccggg gcctgaccg tggtttctt cccggcctga tctgcgcagc 120  
 ccggcgggcg ccagaagga gcaggcggcg cggggcgcg ctggcgggg gaggcgtggc 180  
 cggagctgcg gcgcaagcg ggctgggact gctcgccgc ctctgcccg gcgagcagct 240  
 cagacc atg tcg cct gaa gaa tgg acg tat cta gtg gtt ctt ctt atc 288

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile

1

5

10

tcc atc ccc atc ggc ttc ctc ttt aag aaa gcc ggt cct ggg ctg aag 336

Ser Ile Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys

15

20

25

30

aga tgg gga gca gcc gct gtg ggc ctg ggg ctc acc ctg ttc acc tgt 384

Arg Trp Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys

35

40

45

ggc ccc cac act ttg cat tct ctg gtc acc atc ctc ggg acc tgg gcc 432

Gly Pro His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala

50

55

60

ctc att cag gcc cag ccc tgc tcc tgc cac gcc ctg gct ctg gcc tgg 480

Leu Ile Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp

65

70

75

act ttc tcc tat ctc ctg ttc ttc cga gcc ctc agc ctc ctg ggc ctg 528

Thr Phe Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu

Pro Thr Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu

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95	100	105	110	
aag ctg gtg agc ctg gcc agt gaa gtc cag gac ctg cat ctg gcc cag				624
Lys Leu Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln				
115	120	125		
agg aag gaa atg gcc tca ggc ttc agc aag ggg ccc acc ctg ggg ctg				672
Arg Lys Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu				
130	135	140		
ctg ccc gac gtg ccc tcc ctg atg gag aca ctc agc tac agc tac tgc				720
Leu Pro Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys				
145	150	155		
tac gtg gga atc atg aca ggc ccg ttc ttc cgc tac cgc acc tac ctg				768
Tyr Val Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu				
160	165	170		
gac tgg ctg gag cag ccc ttc ccc ggg gca gtg ccc agc ctg cgg ccc				816
Asp Trp Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro				
175	180	185	190	
ctg ctg cgc cgc gcc tgg ccg gcc ccg ctc ttc ggc ctg ctg ttc ctg				864
Leu Leu Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu				
195	200	205		
ctc tcc tct cac ctc ttc ccg ctg gag gcc gtg cgc gag gac gcc ttc				912
Leu Ser Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe				
210	215	220		
225	230	235		

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ttc gcc ttc cgc atg cgc ttc tac gtg gcc tgg att gcc gcc gag tgc 1008  
 Phe Ala Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys  
 240 245 250  
 ggc tgc att gcc gcc ggc ttt ggg gcc tac ccc gtg gcc gcc aaa gcc 1056  
 Gly Cys Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala  
 255 260 265 270  
 cgg gcc gga ggc ggc ccc acc ctc caa tgc cca ccc ccc agc agt ccg 1104  
 Arg Ala Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro  
 275 280 285  
 gag aag gcg gct tcc ttg gag tat gac tat gag acc atc cgc aac atc 1152  
 Glu Lys Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile  
 290 295 300  
 gac tgc tac agc aca gat ttc tgc gtg cgg gtg cgc gat ggc atg cgg 1200  
 Asp Cys Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg  
 305 310 315  
 tac tgg aac atg acg gtg cag tgg tgg ctg gcg cag tat atc tac aag 1248  
 Tyr Trp Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys  
 320 325 330  
 agc gca cct gcc cgt tcc tat gtc ctg cgc ctt tagaagcaga aactcagcc 1300  
 Ser Ala Pro Ala Arg Ser Tyr Val Leu Arg Leu  
 335 340 345  
 ggggtgcggcg gctcagcct ggaatcccag cactttggga ggcccaagca ggttgatcat 1360  
 gggggggcgg ctgagcccag ggggccagaa ggccctgggac tgggtgcact ggttccctgaa 1540



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gatgcgcgcc tatgactaca tgtgcatggg ctctgtgtg ctctccttgg cgcacacct 1600  
tcggtactgg gcctccatct actttctgtat ccacttctg gccctggcag ccctggggct 1660  
ggggctggct ttaggtgggg gcagccccag ccggcggaag gcagcatccc agcccaccag 1720  
ccttgccccg gagaagctcc gggaggagta agctgtcacg acgtccctc tgccagctgg 1780  
tccccggaat tctgtgaacc aggtgtgtgt ctctcccca gaaagagtc ttaccttgga 1840  
gagggtcctg gagagaattt cctcttcccc agctaaatac cctgcctgca actgaagcag 1900  
acccgggggt gtcctccctg ccctctgccc agaggccacc tccactccta caaatcaaa 1960  
gtattgtcca gacaagagtc actggccctt gctccagctt ctgggtatcc agagagcact 2020  
gcacttcccc aaaacggaag gggcccttgg gcagtgggtt ttgggcaaat tccctttctt 2080  
tgcatccaca atgtggggtc ggagcttggg ggcaggtcct gggagtggga agcctcttcc 2140  
ttgtgtcttt cgtccactt ttagctcatc gcaccaatat tgcagacttg gaaggaagca 2200  
taagcttccc atttcacaaa ggggaaactg aggtgcgggt gcgcgggcct ggggacggcc 2260  
gtcccatggc ttccatctga gccacctcgg gacccagca ctcttggcgc cctcttctca 2320  
tcgcttggcc tatgacaggt caccgtgtgt aaatctttcc caataaagtg ttgcacaaag 2380

&lt;210&gt; 28

&lt;211&gt; 2017

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (360)... (629)

SEQUENCE INFORMATION - CDS (360) - (629) - 120

tgagaatgaa tctgacctca gacccaaatc cattcaacgg agttcttgta atttgaaga 120

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aggaagagca acctggaac tgacaggaaa ggaatgacaag ttgggagtca caggtatatg 180  
 atgggcctcc ccatgtggat ccttagtgct gtggcagagc ccttggttatt gtgctgggat 240  
 ttccctcca gctcccgcc ggaagctggg ctcacgtggg agctcagtgc cctcctgcta 300  
 cagatctgtc tcttccttac aatgggggtgc tggcactgtg ggctcgtgtg acgcacgtg 359  
 atg tac atg caa gat tat tgg agg acc tgg ctc aag ggg ctg cgc ggc 407  
 Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly  
 1 5 10 15  
 ttc ttc ttc gtg ggc gtc ctc ttc teg gcc gtc tcc atc gct gcc ttc 455  
 Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe  
 20 25 30  
 tgc acc ttc ctc gtg ctg gcc atc acc cgg cat cag agc ctc aca gac 503  
 Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp  
 35 40 45  
 ccc acc agc tac tac ctc tcc agc gtc tgg agc ttc att tcc ttc aag 551  
 Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys  
 50 55 60  
 tgg gcc ttc ctg ctc agc ctc tat gcc cac cgc tac cgg gct gac ttt 599  
 Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe  
 65 70 75 80  
 gct gac atc agc atc ctc agc gat ttc tgaccaggg ggtg 640  
 Ala Asp Ile Ser Ile Leu Ser Asp Phe  
 85  
 gtgggtctccc aggaagctgt cctgcccgtc ccttttcgag gaaacctgag tgtggttagag 820

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aggggatcct gccatgttgt tctcatcag cctggccaga gggcagcttt agaccttttc 880  
aatgaatct gttttctttt ctttctttt ttttctttt tttttttt ttgagatgga 940  
gtcttactct gtcaccagg ctggagtga gtagtgcgat ctcagctcac tgcaacctcc 1000  
gcctcccagg ttcaagcaat tctcctgcct tggcctctca agtagctggg attacaggca 1060  
tctgccacca tgcccggcaa atttttgtgt ttttagtaga gacagggtt tgccatgttg 1120  
gccaggctgg tctcgaactc ctgatctcag gtgattcacc cgcctcagcc ttccaaagt 1180  
ctgggattat aggtgtgagc caccgcgcc ggcctggatc tgtttctta gcacgcagtg 1240  
aggaatcttt gtacttaagg ccagggaac aaagtcaaga ggtcaagggt tagggccatg 1300  
aggcctggac ctatgtgca ggcaagggtt tccatccccg ctgccctagg cactctcttc 1360  
ccaaggccag gttgggcacc tggggaggtc agttcagaaa tatctagcag agacctctta 1420  
aacccccatc ccagcaccac atcctgttgt tcccagagct ggtctcccat gagtgtgcta 1480  
gagccagata gccgtggccc cccaccatc tctctcacac acacaggcat ccatacacc 1540  
cagaagactt cccaaatgag gccagactca gggtcacggg gaatgtgett ctgcccctgt 1600  
aagggttttg gggaaggggg caacatagta gaggtggaa agagcccca aacctgtgcc 1660  
catgcccctc cagccctgag tttcattct gccttctcag agtgcccttg ctgcaccag 1720  
accaccggcc aggagagacc ttctctccca ctccagcccc tctcactgcc cttcaactag 1780  
agctttcacc tttttacatt tcccttctga aggacacaaa tctgcttttc tgcccataca 1840  
ctggcccaag ggtcaccta acttgggagg gaaggggctg ttgtacaag gatgatttc 1900  
tgttagactg ccattttgca cggctctccc ctcccatct gatgtgctt gccctcagc 1960  
tctttgectt atctgtgca ctgtcacttt agcaaaaata cagcgccat ttgtatc 2017

&lt;210&gt; 29

SEQUENCE

&lt;213&gt; Homo sapiens

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (30)... (1250)

&lt;400&gt; 29

acctcttccg tcggctgaat tgcggccgt atg cgc ggc tct gtg gag tgc acc	53
Met Arg Gly Ser Val Glu Cys Thr	
1 5	
tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta	101
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu	
10 15 20	
ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag	149
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln	
25 30 35 40	
gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg	197
Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu	
45 50 55	
ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg	245
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp	
60 65 70	
agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc	293
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro	
75 80 85	
90 95 100	

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gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct	389
Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser	
105                      110                      115                      120	
gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc	437
Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser	
125                      130                      135	
gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg	485
Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu	
140                      145                      150	
gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc	533
Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr	
155                      160                      165	
ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act	581
Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr	
170                      175                      180	
ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc	629
Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser	
185                      190                      195                      200	
agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt	677
Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys	
205                      210                      215	
cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc	725
ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc	773

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Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro  
 235 240 245  
 tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc 821  
 Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val  
 250 255 260  
 ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca 869  
 Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala  
 265 270 275 280  
 cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca 917  
 Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser  
 285 290 295  
 gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct 965  
 Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser  
 300 305 310  
 ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac 1013  
 Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn  
 315 320 325  
 ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat 1061  
 Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr  
 330 335 340  
 tgg gac caa cac tac ctc agc tgg tgg atg ctc ctg ggt gtg ggc ttc 1109  
 Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe  
 345 350 355 360  
 Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val

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365	370	375	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg			1205
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu			
380	385	390	
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat taa			1250
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn			
395	400	405	
ggccccgtct ctggagggaa ggacattact gaacctgtct tgctgtgcct cgaaactctg			1310
gaggttgag catcaagttc cagccggccc cttcactccc ccactctgct tttctgtgga			1370
acctcagagg ccagcctcga cttcctggag acccccaggt ggggttccct tcatactttg			1430
ttgggggact ttggaggcgg gcaggggaca gggctattga taaggtcccc ttggtgttgc			1490
cttcttgcat ctccacacat ttcccttga tgggacttgc aggcctaaat gagaggcatt			1550
ctgactggtt ggctgccctg gaaggcaaga aaatagattt attttttttc acaggg			1606

&lt;210&gt; 30

&lt;211&gt; 1695

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (53)... (631)

&lt;400&gt; 30

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act gcc gtc ggc gtg cag gcc cag agg cct ttg ggc caa agg cag ccc	103
Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro	
5 10 15	
cgc cgg tcc ttc ttt gaa tcc ttc atc cgg acc ctc atc atc acg tgt	151
Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys	
20 25 30	
gtg gcc ctg gct gtg gtc ctg tcc tgc gtc tcc att tgt gat ggg cac	199
Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His	
35 40 45	
tgg ctc ctg gct gag gac cgc ctc ttc ggg ctc tgg cac ttc tgc acc	247
Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr	
50 55 60 65	
acc acc aac cag agt gtg ccg atc tgc ttc aga gac ctg ggc cag gcc	295
Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala	
70 75 80	
cat gtg ccc ggg ctg gcc gtg ggc atg ggc ctg gta cgc agc gtg ggc	343
His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly	
85 90 95	
gcc ttg gcc gtg gtg gcc gcc att ttt ggc ctg gag ttc ctc atg gtg	391
Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val	
100 105 110	
tcc cag ttg tgc gag gac aaa cac tca cag tgc aag tgg gtc atg ggt	439
tcc atc ctc ctc ctg gtg tct ttc gtc ctc tcc tcc ggc ggg ctc ctg	487



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Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu  
 130 135 140 145  
 ggt ttt gtg atc ctc ctc agg aac caa gtc aca ctc atc ggc ttc acc 535  
 Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr  
 150 155 160  
 cta atg ttt tgg tgc gaa ttc act gcc tcc ttc ctc ctc ttc ctg aac 583  
 Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn  
 165 170 175  
 gcc atc agc ggc ctt cac atc aac agc atc acc cat ccc tgg gaa tg 630  
 Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu  
 180 185 190  
 accgtgaaa ttttaggcc cctccaggga catcagattc cacaagaaaa tatggtcaaa 690  
 atgggacttt tccagcatgt ggcctctggt ggggctgggt tggacaaggg ccttgaaacg 750  
 gtgacctgtt tgccgataac ttgtgggtgg tcagccagaa atggcccggg ggcctctgca 810  
 cctggtctgc aggccagag gccaggaggg tgcctcagt ccaccaactg cacaggctta 870  
 gccagatgtt gattttagag gaagaaaaaa acattttaaa actccttctt gaattttctt 930  
 ccctggactg gaatacagtt ggaagcacag gggtaactgg tacctgagct agctgcacag 990  
 ccaaggatag ttcatgcctg ttccattgac acgtgctggg ataggggctg cagaatccct 1050  
 ggggctccca gggttgttaa gaatggatca ttcttcagc taagggtcca atcagtgcct 1110  
 attctccac cagctcaaag ggccttcgta tgtatgtccc tggcttcagc tttggtcatg 1170  
 ccaaagaggc agagttcagg attccctcag aatgccctgc acacagtagg ttccaaacc 1230  
 atttgactcg gtttgccctc ctgcccgttg tttaaaccctt acaaaccctg gataacccca 1290  
 aatacacagc cctccccaag gcccggtgtg gcatgtgtct gtcttttctg agggtttagc 1470

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agcctcaggg caccattttt aatcccagaa cacatttcaa agagcacgta tctagacctg 1530  
 ctggactctg cagggggtga gggggaacag cgagagcttg ggtaatgatt aacacccatg 1590  
 ctggggatgc atggaggtga agggggccag gaaccagtgg agatttccat ccttgccagc 1650  
 acgtctgtac ttctgttcat taaagtgtc cctttctagt ccttt 1695

&lt;210&gt; 31

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

1                      5                      10                      15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

20                      25                      30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

35                      40                      45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

50                      55                      60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

65                      70                      75                      80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

85                      90                      95

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

68 / 307

115	120	125	
Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln			
130	135	140	
Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr			
145	150	155	160
Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr			
165	170	175	
Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe			
180	185	190	
Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly			
195	200	205	
Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe			
210	215	220	
Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile			
225	230	235	240
Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn			
245	250	255	
Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe			
260	265	270	
Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His			
275	280	285	
Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu			
305	310	315	320

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Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala

325

330

335

Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys

340

345

350

Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala

355

360

365

Ser Lys Gly Leu Glu Lys Lys Glu Lys

370

375

&lt;210&gt; 32

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

Met Thr Ala His Ser Phe Ala Leu Pro Val Ile Ile Phe Thr Thr Phe

1

5

10

15

Trp Gly Leu Val Gly Ile Ala Gly Pro Trp Phe Val Pro Lys Gly Pro

20

25

30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Ala Thr Ala Val Cys Cys

35

40

45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

50

55

60

Glu

70 /307

&lt;210&gt; 33

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu Lys Ser Ile

1 5 10 15

Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu Leu Gly Leu

20 25 30

Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly Ser Gly Ile

35 40 45

Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala Val Gly Pro

50 55 60

Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr Leu Gly Ala

65 70 75 80

Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser Gly Gly Glu

85 90 95

Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala Tyr Leu Phe

100 105 110

Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe Ala Ile Ile

130

135

140

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Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala Ala Ile Leu

145 150 155 160

Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly Ser Tyr Val

165 170 175

Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala Ile Ile Ile

180 185 190

Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys Asn Phe Asp

195 200 205

Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile Ser Leu Ala

210 215 220

Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln Leu Asn Tyr

225 230 235 240

Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile

245 250 255

Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu Met Asn Val

260 265 270

Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln Ser Gln Ala

275 280 285

Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala Ser Trp Ile

290 295 300

Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala Asn Gly Thr

305 310 315 320

Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu Thr Pro Ala

72 /307

340 345 350  
Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr Ile Ile Pro  
355 360 365  
Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala Ala Trp Leu  
370 375 380  
Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg Phe Thr Arg  
385 390 395 400  
Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile Pro Val Leu  
405 410 415  
Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile Ile Ser Lys  
420 425 430  
Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu Ser Gly Leu  
435 440 445  
Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp Ala Gln Lys  
450 455 460  
Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met Glu Val Val  
465 470 475 480  
Pro Pro Glu Glu Asp Pro Glu  
485

&lt;210&gt; 34

&lt;211&gt; 375

&lt;212&gt; PPT

&lt;400&gt; 34

73 /307

Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val

1 5 10 15

Val Ala Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu

20 25 30

Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg

35 40 45

Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln

50 55 60

Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala

65 70 75 80

Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val

85 90 95

Phe Ser Ala Phe Ala Ser Gly Leu Leu His Leu Tyr Leu Gly Leu Gly

100 105 110

Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly

115 120 125

Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu

130 135 140

Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu

145 150 155 160

Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu

165 170 175

Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val

Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala



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195	200	205	
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala			
210	215	220	
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His			
225	230	235	240
Leu Ala Pro Arg Phe Arg Pro Gly Pro Gly Gly Ile Arg Ser Ser Ala			
245	250	255	
Gly Gly Gly Arg Gly Cys Asp Gly Gly Cys Gly Arg Pro Ala Gly Leu			
260	265	270	
Arg Val Ala Gly Arg Pro Arg Leu Gly Ala Pro Pro Ala Ala Ala Gly			
275	280	285	
Arg Ile Arg Gly Ser Asp Trp Ala Gly Ala Val Gly Gly Gly Ala Gly			
290	295	300	
Ala Arg Gly Gly Arg Arg Arg Glu Leu Gly Gly Ser Pro Ala Gly Arg			
305	310	315	320
Gly Cys Gly Leu Trp Ala Glu Arg Gly Glu Leu Arg Pro Ala Gly Phe			
325	330	335	
Arg Cys Thr Pro Arg Ala Gly Gly Arg Arg Arg Cys Gly Ala Gly His			
340	345	350	
Arg Ala Gly Asp Asp Ala Asp Glu Pro Arg Gly Ala Pro Gly Pro Ser			
355	360	365	
Pro Val Arg Leu Pro Lys Gly			

75 / 307

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly

1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala

20 25 30

Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu

35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala

50 55 60

Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu

65 70 75 80

Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln

85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr

100 105 110

Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln

115 120 125

Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn

130 135 140

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

76 / 307

165	170	175	
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe			
180	185	190	
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu			
195	200	205	
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr			
210	215	220	
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His			
225	230	235	240
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser			
245	250	255	
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr			
260	265	270	
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe			
275	280	285	
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu			
290	295	300	
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg			
305	310	315	320
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu			
325	330	335	
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His			

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&lt;211&gt; 667

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu

1 5 10 15

Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu

20 25 30

Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro

35 40 45

Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu

50 55 60

Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys

65 70 75 80

Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly

85 90 95

Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser

100 105 110

Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr

115 120 125

Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly

130 135 140

Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly

78 /307

165	170	175	
Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala			
180	185	190	
Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala			
195	200	205	
Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro			
210	215	220	
Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys			
225	230	235	240
Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys			
245	250	255	
Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu			
260	265	270	
Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro			
275	280	285	
Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly			
290	295	300	
Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro			
305	310	315	320
Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu			
325	330	335	
Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val			
340	345	350	
355	360	365	

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Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser

370

375

380

Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala

385

390

395

400

Leu Asp Leu Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala

405

410

415

Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys

420

425

430

Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala

435

440

445

Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn Leu Leu

450

455

460

Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr Leu Ala

465

470

475

480

Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu

485

490

495

Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu Tyr Ala

500

505

510

Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala Met Val

515

520

525

Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu

530

535

540

Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln

Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln

80 / 307

565	570	575	
Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln			
580	585	590	
Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro			
595	600	605	
Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met			
610	615	620	
Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly Arg Ala Arg Trp Gly			
625	630	635	640
Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys			
645	650	655	
Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro			
660	665		

&lt;210&gt; 37

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

Met Ile Val Cys Leu Leu Phe Met Met Ile Leu Leu Ala Lys Glu Val
1                      5                      10                      15
Gln Leu Val Asp Gln Thr Asp Ser Pro Leu Leu Ser Leu Leu Gly Gln

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Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu Ala

50

55

60

Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val Ser Ala

65

70

75

80

Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp Ala Val Pro

85

90

95

Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe Leu Ser Thr Leu

100

105

110

Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu Glu Gln Glu Met Ser

115

120

125

Lys Leu Leu Asp Asp Ile Ile Val Phe Asn Pro Pro Asp Met Asp Ser

130

135

140

Gln Thr Arg His Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met

145

150

155

160

Met Met Asn Asn Ala Thr Ile Pro Thr Ala Glu Phe Leu Arg Gly Ser

165

170

175

Ile Arg Thr Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro

180

185

190

Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala Ser Val Arg His Met Ala

195

200

205

Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu

210

215

220

Glu Leu Thr Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser



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245	250	255	
Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln			
260	265	270	
Thr Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu			
275	280	285	
Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe Leu			
290	295	300	
Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu Gln Asn			
305	310	315	320
Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu Leu Val Gln			
325	330	335	
Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser Ser Gly Ile Leu			
340	345	350	
Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu Ser Asn Arg Phe Arg			
355	360	365	
Val Val Ala Arg Ser Met Ala Ala Phe Leu Ser Val Gln Val Pro Met			
370	375	380	
Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser Glu Leu His Leu Thr Pro			
385	390	395	400
Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu Ser Met Ala Ser Ser Lys			
405	410	415	
Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu Gln Ala Thr Gln Phe Ile			
435	440	445	

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Leu Val Asn Cys Leu Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg

450

455

460

&lt;210&gt; 38

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu

1

5

10

15

Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser

20

25

30

Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro

35

40

45

Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met

50

55

60

Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

65

70

75

80

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

85

90

95

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg

100

105

110

His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Phe Pro Phe

84 / 307

130	135	140	
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr			
145	150	155	160
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr			
	165	170	175
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu			
	180	185	190
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly			
	195	200	205
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser			
	210	215	220
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro			
225	230	235	240
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys			
	245	250	255
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser			
	260	265	270
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys			
	275	280	285
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly			
	290	295	300
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp			

325

330

335

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Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val

340

345

350

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

355

360

365

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

370

375

380

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385

390

395

400

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

405

410

415

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

420

425

430

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

435

440

445

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

450

455

460

Glu Val Ile Leu Arg Asp

465

470

&lt;210&gt; 39

&lt;211&gt; 243

&lt;212&gt; PRT

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe

86 / 307

1	5	10	15
Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp			
20	25	30	
Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly			
35	40	45	
Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly			
50	55	60	
Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser			
65	70	75	80
Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu			
85	90	95	
Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu			
100	105	110	
Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro			
115	120	125	
Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr			
130	135	140	
Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val			
145	150	155	160
Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met			
165	170	175	
Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala			

195

200

205

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Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu

210

215

220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser

225

230

235

240

Leu Pro Arg

&lt;210&gt; 40

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

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1

5

10

15

Asp Glu Ala Ser Cys Cys Arg Trp Gly Ala Gln His Ala Gly Ala Arg

20

25

30

Glu Leu Ala Ala Leu Tyr Ser Pro Gly Lys Arg Leu Gln Glu Trp Cys

35

40

45

Ser Val Ile Leu Cys Phe Ser Leu Ile Ala His Asn Leu Val His Leu

50

55

60

Leu Leu Leu Ala Arg Trp Glu Asp Thr Pro Leu Val Ile Leu Gly Val

65

70

75

80

Val Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His Trp

100

105

110

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Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile Thr

115

120

125

Arg His Asp Phe Ile Glu Thr Asn Gly Asp Asn Cys Leu Val Thr Leu

130

135

140

Leu Pro Leu Leu Asn Met Ala Tyr Lys Phe Arg Thr His Ser Pro Glu

145

150

155

160

Ala Leu Glu Gln Leu Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile

165

170

175

Ile Phe Gly Thr Phe Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr

180

185

190

Phe Gly Leu Pro Arg Trp Val Thr Leu Leu Gln Asp Trp His Val Ile

195

200

205

Leu Pro Arg Lys His His Arg Ile His His Val Ser Pro His Glu Thr

210

215

220

Tyr Phe Cys Ile Thr Thr Gly Trp Leu Asn Tyr Pro Leu Glu Lys Ile

225

230

235

240

Gly Phe Trp Arg Arg Leu Glu Asp Leu Ile Gln Gly Leu Thr Gly Glu

245

250

255

Lys Pro Arg Ala Asp Asp Met Lys Trp Ala Gln Lys Ile Lys

260

265

270

&lt;210&gt; 41

111 118

&lt;213&gt; Homo sapiens

89 / 307

&lt;400&gt; 41

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&lt;210&gt; 42

&lt;211&gt; 212

&lt;213&gt; Homo sapiens



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&lt;400&gt; 42

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&lt;210&gt; 43

&lt;211&gt; 1461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

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 ccaccggagg aagaccctga g 1461

&lt;210&gt; 44

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

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&lt;210&gt; 45

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

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&lt;210&gt; 46

&lt;211&gt; 2001

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

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ggtgccaatg gtgcccagcc c

2001

&lt;210&gt; 47

&lt;211&gt; 1392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

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&lt;210&gt; 48

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

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&lt;210&gt; 49

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

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 ctccctcgc 729

&lt;210&gt; 50

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

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&lt;210&gt; 51

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (98)... (1231)

&lt;400&gt; 51

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accggagctg gagtcggatc ccgaacgcac cctcgcc atg gac tcg gcc etc agc 115

Met Asp Ser Ala Leu Ser

1 5

gat ccg cat aac ggc agt gcc gag gca ggc ggc ccc acc aac agc act 163

Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly Pro Thr Asn Ser Thr

10 15 20

acg cgg ccg cct tcc acg ccc gag ggc atc gcg ctg gcc tac ggc agc 211

Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala Leu Ala Tyr Gly Ser

25 30 35

etc ctg etc atg gcg ctg ctg ccc atc ttc ttc ggc gcc ctg cgc tcc 259

Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser

40 45 50

60 65 70

55

60

65

70

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acc agc cgg gat gcc gcc cgc ttc ccc atc atc gcc agc tgc aca ctc	355
Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu	
75 80 85	
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Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn	
90 95 100	
ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga atc ctg gcc ctg tcc	451
Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser	
105 110 115	
cac acc atc agc ccc ttc atg aat aag ttt ttt cca gcc agc ttt cca	499
His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro	
120 125 130	
aat cga cag tac cag ctg ctc ttc aca cag ggt tct ggg gaa aac aag	547
Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys	
135 140 145 150	
gaa gag atc atc aat tat gaa ttt gac acc aag gac ctg gtg tgc ctg	595
Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu	
155 160 165	
ggc ctg agc agc atc gtt ggc gtc tgg tac ctg ctg agg aag cac tgg	643
Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp	
170 175 180	
att gcc aac aac ctt ttt ggc ctg gcc ttc tcc ctt aat gga gta gag	691
ctc ctg cac ctc aac aat gtc agc act ggc tgc atc ctg ctg ggc gga	739

101/307

Leu Leu His Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly  
 200 205 210  
 ctc ttc atc tac gat gtc ttc tgg gta ttt ggc acc aat gtg atg gtg 787  
 Leu Phe Ile Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val  
 215 220 225 230  
 aca gtg gcc aag tcc ttc gag gca cca ata aaa ttg gtg ttt ccc cag 835  
 Thr Val Ala Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln  
 235 240 245  
 gat ctg ctg gag aaa ggc ctc gaa gca aac aac ttt gcc atg ctg gga 883  
 Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly  
 250 255 260  
 ctt gga gat gtc gtc att cca ggg atc ttc att gcc ttg ctg ctg cgc 931  
 Leu Gly Asp Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg  
 265 270 275  
 ttt gac atc agc ttg aag aag aat acc cac acc tac ttc tac acc agc 979  
 Phe Asp Ile Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser  
 280 285 290  
 ttt gca gcc tac atc ttc ggc ctg ggc ctt acc atc ttc atc atg cac 1027  
 Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His  
 295 300 305 310  
 atc ttc aag cat gct cag cct gcc ctc cta tac ctg gtc ccc gcc tgc 1075  
 Ile Phe Lys His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys  
  
 Ile Gly Phe Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu

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330	335	340	
atg ttc agt tat gag gag tca aat cct aag gat cca gcg gca gtg aca			1171
Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr			
345	350	355	
gaa tcc aaa gag gga aca gag gca tca gca tcg aag ggg ctg gag aag			1219
Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys			
360	365	370	
aaa gag aaa tg atgcagctgg tgcccgagcc tctcagggcc agaccagaca			1270
Lys Glu Lys			
375			
gatgggggct gggcccacac aggcgtgcac cggtagaggg cacaggaggc caagggcagc			1330
tccaggacag ggcagggggc agcaggatac ctccagccag gcctctgtgg cctctgtttc			1390
cttctccctt tcttgccct cctctgctcc tccccacacc ctgcaggcaa aagaaacccc			1450
cagcttcccc cctccccggg agccaggtgg gaaaagtggg tgtgattttt agattttgta			1510
ttgtggactg attttgcctc acattaaaaa ctcatcccat g			1551

&lt;210&gt; 52

&lt;211&gt; 1713

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

tctcagcggc ctgcccggct ggggacccgc gcacctgcag cgcgccgtgc tggccctgc 60

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atcctgcctg ggcatcctgc gcccggcc atg acg gcg cac tca ttc gcc ctc 112

Met Thr Ala His Ser Phe Ala Leu

1

5

ccg gtc atc atc ttc acc acg ttc tgg ggc ctc gtc ggc atc gcc ggg 160

Pro Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly

10

15

20

ccc tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg 208

Pro Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met

25

30

35

40

ctg gtc gcc acc gcc gtc tgc tgt tac ctc ttc tgg ctc atc gcc atc 256

Leu Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile

45

50

55

ctg gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc 304

Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr

60

65

70

atc tgg tac gtg cgc ttc ctg tgg gag tgacccgcc gccccgcacc 350

Ile Trp Tyr Val Arg Phe Leu Trp Glu

75

80

caggtgccca gctctcgga tgaactgtgc tcaactgtcc ctgacaaccc ctctgtccgg 410

accctccccc acacaactat gtctgggtcac cagctccctc ctgctggcac ccagagaccc 470

ggaccgcag ggctgcctg gtctctggaa gtcttccag tcttccagc cagcccgggc 530

cctggggagc cctgggcaca gcagcgccg aggggatgtc ctgtccaat accgcactg 590

ctcatggaga ggggtgctccg gcccgaggcg gggagtcagt gccagtcag cagctctgcc 770

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accatcctgc tgggaactgg gggggcctct attgggttat aggcaaggcc ttttctctgg 830  
 catggaattg ttaattttct gacacgtcta gatgtgaaat ttctgaaaat gttgaagcag 890  
 agaaacattc acacacaaaa agcaacatag tcatgtgggt ccagatggcc tcagtcctag 950  
 atgttggcac cctttgctgt gtctctcag agtatcctgt tccgcctcct gccacctgga 1010  
 cctccctcag tggatgtctt cctcccccgc accccagcct gtcagtccga gcacagtga 1070  
 ggtttggctc tgacttgggc ttttggctgc agtgggggtg gatttcagag cctctcatgg 1130  
 cagcatctaa gtgaccagag ctgggatgag agaggggaag gggcaatgtg agtggcgcta 1190  
 tgggacgggc cagccctgct cctgagccag ccccgccctc tgccccctgg ccttgggctc 1250  
 tgtgctaggg atggtgaaga atgggggcgt gccagcctgg caggagtggg aagcaacacg 1310  
 caggggtccc ggacctctcc agccttgcct tcacgcttac ccgagctccc agtgttggtta 1370  
 gcacagagct caccacctt gcctggctcc cagctggggc ctgtctcac tgggtgctcca 1430  
 ggggaagaaa cgacagctc acttctgtat ggactgctga tgtggcctgc catcctgttc 1490  
 agcgggcatt gtctttggag cagcaggaga ataggatgcc tctcactcac atgccagttc 1550  
 ctggetggcc agctgctcag ggctcaggct ggggcctccc attgacatcc tccccctaca 1610  
 ctccctctct gagcctccgt cggccctcct gttgggtaag ggtgttgagt gtgacttggt 1670  
 ctgaaaacct ggttcataata taataaataa tggtgatgaa aag 1713

&lt;210&gt; 53

&lt;211&gt; 1758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

· 400 · 53

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tttctagggg	tggaccgtgc	aggcacgggc	ggtcagctgg	gccgcagctc	ctccggctct	60
gcagggtcac	ggaggaagcc	agctccccta	gtccaggccg	agcttgcaact	tgcgtcttgt	120
ctgctgctgc	tgaaccaaga	tttagctgtg	cgccctcctt	gcagtctcct	ggaaccagca	180
ggaggaaac	atg ggg	gat act	ggc ctg	aga aag	cgg aga	228
Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu						
1	5	10				
aag tgc	atc cag	agc caa	gag cct	aag acc	acc agt	276
Lys Ser	Ile Gln	Ser Gln	Glu Pro	Lys Thr	Thr Ser	
15	20	25				
ctg ggc	ctc atc	agt ggc	atc tcc	atc atc	gtg ggc	324
Leu Gly	Leu Ile	Ser Gly	Ile Ser	Ile Ile	Val Gly	
30	35	40	45			
tct ggg	atc ttc	gtt tcc	ccc aag	tct gtg	ctc agc	372
Ser Gly	Ile Phe	Val Ser	Pro Lys	Ser Val	Leu Ser	
50	55	60				
gtg ggg	ccc tgc	ctc atc	ata tgg	gcg gct	tgc ggg	420
Val Gly	Pro Cys	Leu Ile	Ile Trp	Ala Ala	Cys Gly	
65	70	75				
ctg ggt	gcc ctg	tgc ttt	gcg gag	ctt ggc	aca atg	468
Leu Gly	Ala Leu	Cys Phe	Ala Glu	Leu Gly	Thr Met	
80	85	90				
ggg gga	gag tat	ccc tac	ctg atg	gag gcc	tac ggg	516
tac ctc	ttc tcc	tgg gcc	agc ctg	atc gtc	att aag	564



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Tyr Leu Phe Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe  
 110 115 120 125  
 gcc atc atc tgc ctc agc ttc tcc gag tat gtg tgt gcg ccc ttc tat 612  
 Ala Ile Ile Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr  
 130 135 140  
 gtg ggc tgc aag cct cct caa atc gtt gtg aaa tgc ctg gcc gcc gcc 660  
 Val Gly Cys Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala  
 145 150 155  
 gcc atc ttg ttc atc tcg aca gtg aac tca ctg agc gtg cgg ctg gga 708  
 Ala Ile Leu Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly  
 160 165 170  
 agc tac gtc cag aac atc ttc acc gcg gcc aag ctg gtg atc gtg gcc 756  
 Ser Tyr Val Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala  
 175 180 185  
 atc atc atc atc agc ggg ctg gtg ctc ctg gcc caa gga aac aca aag 804  
 Ile Ile Ile Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys  
 190 195 200 205  
 aat ttt gat aat tct ttc gag ggc gcc cag ctg tct gtg gga gcc atc 852  
 Asn Phe Asp Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile  
 210 215 220  
 agc ctg gcg ttt tac aat gga ctc tgg gcc tat gat gga tgg aat caa 900  
 Ser Leu Ala Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln  
  
 Leu Asn Tyr Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro

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240	245	250	
ttg gcc att atc atc ggg atc ccc ctg gtg acg gcg tgc tac atc ctc			996
Leu Ala Ile Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu			
255	260	265	
atg aac gtg tcc tac ttc acc gtg atg act gcc acc gaa ctc ctg cag			1044
Met Asn Val Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln			
270	275	280	285
tcc cag gcg gtg gct gtg aca ttt ggt gac cgt gtt ctc tat cct gct			1092
Ser Gln Ala Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala			
290	295	300	
tct tgg atc gtt cca ctt ttt gtg gca ttt tca acc atc ggt gct gct			1140
Ser Trp Ile Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala			
305	310	315	
aac ggg acc tgc ttc aca gcg ggc aga ctc att tac gtg gcg ggc cgg			1188
Asn Gly Thr Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg			
320	325	330	
gag ggt cac atg ctc aaa gtg ctt tct tac atc agc gtc agg cgc ctc			1236
Glu Gly His Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu			
335	340	345	
act cca gcc ccc gcc atc atc ttt tat ggt atc ata gca acg att tat			1284
Thr Pro Ala Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr			
350	355	360	365
370	375	380	

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gca tgg ctg ttt tat ggc ctg acg att cta gga ctc atc gtg atg aga 1380  
 Ala Trp Leu Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg  
 385 390 395  
 ttt aca agg aaa gag ctg gaa agg cct atc aag gtg ccc gta gtc att 1428  
 Phe Thr Arg Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile  
 400 405 410  
 ccc gtc ttg atg aca ctc atc tct gtg ttt ttg gtt ctg gct cca atc 1476  
 Pro Val Leu Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile  
 415 420 425  
 atc agc aag ccc acc tgg gag tac ctc tac tgt gtg ctg ttt ata tta 1524  
 Ile Ser Lys Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu  
 430 435 440 445  
 agc ggc ctt tta ttt tac ttc ctg ttt gtc cac tac aag ttt gga tgg 1572  
 Ser Gly Leu Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp  
 450 455 460  
 gct cag aaa atc tca aag ccg att acc atg cac ctt cag atg cta atg 1620  
 Ala Gln Lys Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met  
 465 470 475  
 gaa gtg gtc cca ccg gag gaa gac cct gag taacaagetc cgtctcttgt 1670  
 Glu Val Val Pro Pro Glu Glu Asp Pro Glu  
 480 485  
 agccaagtca gctgaattta tttcttaag caatatttgt gggtatttct tcttttttt 1730

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&lt;211&gt; 1550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (154)... (1281)

&lt;400&gt; 54

ctctgtttac cgagagagcc cgtccaagtt gggtccatc gctgccctcg ctccccttcg	60
gggcctccgc ccgcctggga agcagagaga aagccgggccc cagcccttcc tcacccttcc	120
cctccccgca ccgcccggag aggtcggacg gcg atg acc ccc cag ccc gcc gga	174
Met Thr Pro Gln Pro Ala Gly	
1 5	
ccc ccg gat ggg ggc tgg ggc tgg gtg gtg gcg gcc gca gcc ttc gcg	222
Pro Pro Asp Gly Gly Trp Gly Trp Val Val Ala Ala Ala Ala Phe Ala	
10 15 20	
ata aac ggg ctg tcc tac ggg ctg ctg cgc tcg ctg ggc ctt gcc ttc	270
Ile Asn Gly Leu Ser Tyr Gly Leu Leu Arg Ser Leu Gly Leu Ala Phe	
25 30 35	
cct gac ctt gcc gag cac ttt gac cga agc gcc cag gac act gcg tgg	318
Pro Asp Leu Ala Glu His Phe Asp Arg Ser Ala Gln Asp Thr Ala Trp	
40 45 50 55	
atc agc gcc ctg gcc ctg gcc gtg cag cag gca gcc agc ccc gtg ggc	366
agc gcc ctg agc acg cgc tgg ggg gcc cgc ccc gtg gtg atg gtt ggg	414

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Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly  
                     75                    80                    85  
 ggc gtc ctc gcc tcg ctg ggc ttc gtc ttc tcg gct ttc gcc agc ggt 462  
 Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe Ala Ser Gly  
                     90                    95                    100  
 ctg ctg cat ctc tac ctc ggc ctg ggc ctc ctc gct ggc ttt ggt tgg 510  
 Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly Phe Gly Trp  
                     105                    110                    115  
 gcc ctg gtg ttc gcc ccc gcc cta ggc acc ctc tcg cgt tac ttc tcc 558  
 Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg Tyr Phe Ser  
                     120                    125                    130                    135  
 cgc cgt cga gtc ttg gcg gtg ggg ctg gcg ctc acc ggc aac ggg gcc 606  
 Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly Asn Gly Ala  
                     140                    145                    150  
 tcc tcg ctg ctc ctg gcg ccc gcc ttg cag ctt ctc ctc gat act ttc 654  
 Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu Asp Thr Phe  
                     155                    160                    165  
 ggc tgg cgg ggc gct ctg ctc ctc ctc ggc gcg atc acc ctc cac ctc 702  
 Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr Leu His Leu  
                     170                    175                    180  
 acc ccc tgt ggc gcc ctg ctg cta ccc ctg gtc ctt cct gga gac ccc 750  
 Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro Gly Asp Pro  
  
 Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu Ser Leu Phe



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ggg cgt cgg agg tgt ggt gca ggc cac agg gct ggt gat gat gct gat 1230

Gly Arg Arg Arg Cys Gly Ala Gly His Arg Ala Gly Asp Asp Ala Asp

345

350

355

gag cct cgg ggg gct cct ggg ccc tcc cct gtc agg ctt cct aag gga 1278

Glu Pro Arg Gly Ala Pro Gly Pro Ser Pro Val Arg Leu Pro Lys Gly

360

365

370

375

tg agacaggaga cttcacggcc tctttcctcc tgtctggttc ttgatactc 1330

tccggcagct tcactacat agggttgcc agggcgctgc cctcctgtgg tccagcctcc 1390

cctccagcca cgctccccc agagacgggg gagctgcttc ccgtcccca ggcagtcttg 1450

ctgtccccag gaggcctgg ctccactctg gacaccactt gttgattatt ttcttgttg 1510

agccccctcc ccaataaaga atttttatcg ggttttcctg 1550

<210> 55

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)... (1153)

<400> 55

ctctcctga ccttgacgt ctaccttcg gaggccaca tcttgccac tccgcgcgcg 60

gggctagcgc gggtttcagc gacgggagcc ctcaaggagc atg gca act aca gcg 115

115 115 115 115 115 115

gcg ccg gcg ggc ggc gcc cga aat gga gct ggc ccg gaa tgg gga ggg 163

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Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly Pro Glu Trp Gly Gly  
10 15 20  
ttc gaa gaa aac atc cag ggc gga ggc tca gct gtg att gac atg gag 211  
Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala Val Ile Asp Met Glu  
25 30 35  
aac atg gat gat acc tca ggc tct agc ttc gag gat atg ggt gag ctg 259  
Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu Asp Met Gly Glu Leu  
40 45 50  
cat cag cgc ctg cgc gag gaa gaa gta gac gct gat gca gct gat gca 307  
His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala Asp Ala Ala Asp Ala  
55 60 65  
gct gct gct gaa gag gag gat gga gag ttc ctg ggc atg aag ggc ttt 355  
Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys Gly Phe  
70 75 80 85  
aag gga cag ctg agc cgg cag gtg gca gat cag atg tgg cag gct ggg 403  
Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln Ala Gly  
90 95 100  
aaa aga caa gcc tcc agg gcc ttc agc ttg tac gcc aac atc gac atc 451  
Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile Asp Ile  
105 110 115  
ctc aga ccc tac ttt gat gtg gag cct gct cag gtg cga agc agg ctc 499  
Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser Arg Leu  
Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln Lys Ile



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135	140	145	
gca ggt gaa ctc tat gga cct ctc atg ctg gtc ttc act ctg gtt gct			595
Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala			
150	155	160	165
atc cta ctc cat ggg atg aag acg tct gac act att atc cgg gag ggc			643
Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly			
	170	175	180
acc ctg atg ggc aca gcc att ggc acc tgc ttc ggc tac tgg ctg gga			691
Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly			
	185	190	195
gtc tca tcc ttc att tac ttc ctt gcc tac ctg tgc aac gcc cag atc			739
Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile			
200	205	210	
acc atg ctg cag atg ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat			787
Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His			
215	220	225	
tgc att gtc ctg ttc atc acc tat aat atc cac ctc cac gcc ctc ttc			835
Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala Leu Phe			
230	235	240	245
tac ctc ttc tgg ctg ttg gtg ggt gga ctg tcc aca ctg cgc atg gta			883
Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val			
	250	255	260
			921
265	270	275	

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tgt ggc acc ctg gct gcc cta cac atg ctc ttc ctg ctc tat ctg cat	979
Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr Leu His	
280 285 290	
ttt gcc tac cac aaa gtg gta gag ggg atc ctg gac aca ctg gag ggc	1027
Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu Glu Gly	
295 300 305	
ccc aac atc ccg ccc atc cag agg gtc ccc aga gac atc cct gcc atg	1075
Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met	
310 315 320 325	
ctc cct gct gct cgg ctt ccc acc acc gtc ctc aac gcc aca gcc aaa	1123
Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys	
330 335 340	
gct gtt gcg gtg acc ctg cag tca cac tgaccccacc tgaaattctt	1170
Ala Val Ala Val Thr Leu Gln Ser His	
345 350	
ggccagtcct ctttcccgca gctgcagaga ggaggaagac tattaaagga cagtcctgat	1230
gacatgtttc gtagatgggg tttgcagctg ccactgagct gtagctgcgt aagtacctcc	1290
ttgatgcctg teggcacttc tgaaaggcac aaggccaaga actcctggcc aggactgcaa	1350
ggctctgcag ccaatgcaga aaatgggtca gctcctttga gaacctctcc ccacctaccc	1410
cttccttcct ctttatctct cccacattgt cttgctaaat atagacttgg taattaaaat	1470
gttgattgaa gtctg	1485

&lt;212&gt; DNA

116/307

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (80)... (2083)

&lt;400&gt; 56

gtagactctg cggatcccga gaccagcgcc actcatcctg cagcactggg gacagacaga	60
gcaggagaag ggccagaga atg tcg tcc cag cca gca ggg aac cag acc tcc	112
Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser	
1 5 10	
ccc ggg gcc aca gag gac tac tcc tat ggc agc tgg tac atc gat gag	160
Pro Gly Ala Thr Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu	
15 20 25	
ccc cag ggg ggc gag gag ctc cag cca gag ggg gaa gtg ccc tcc tgc	208
Pro Gln Gly Gly Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys	
30 35 40	
cac acc agc ata cca ccc ggc ctg tac cac gcc tgc ctg gcc tcg ctg	256
His Thr Ser Ile Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu	
45 50 55	
tea atc ctt gtg ctg ctg ctc ctg gcc atg ctg gtg agg cgc cgc cag	304
Ser Ile Leu Val Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln	
60 65 70 75	
ctc tgg cct gac tgt gtg cgt ggc agg ccc ggc ctg ccc agc cct gtg	352
gat ttc ttg gct ggg gac agg ccc egg gca gtg cct gct gct gtt ttc	400

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Asp Phe Leu Ala Gly Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe  
                   95                  100                  105  
 atg gtc ctc ttg agc tcc ctg tgt ttg ctg ctc ccc gac gag gac gca 448  
 Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala  
                   110                  115                  120  
 ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat ggg aaa act 496  
 Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr  
                   125                  130                  135  
 gag gct cca aga ggg gcc tgg aag ata ctg gga ctg ttc tat tat gct 544  
 Glu Ala Pro Arg Gly Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala  
                   140                  145                  150                  155  
 gcc ctc tac tac cct ctg gct gcc tgt gcc acg gct ggc cac aca gct 592  
 Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala  
                   160                  165                  170  
 gca cac ctg ctc ggc agc acg ctg tcc tgg gcc cac ctt ggg gtc cag 640  
 Ala His Leu Leu Gly Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln  
                   175                  180                  185  
 gtc tgg cag agg gca gag tgt ccc cag gtg ccc aag atc tac aag tac 688  
 Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr  
                   190                  195                  200  
 tac tcc ctg ctg gcc tcc ctg cct ctc ctg ctg ggc ctc gga ttc ctg 736  
 Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu  
  
 Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr

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220	225	230	235	
gga gca ggc tcc aag ggg ctg cag agc agc tac tct gag gaa tat ctg				832
Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu				
240	245	250		
agg aac ctc ctt tgc agg aag aag ctg gga agc agc tac cac acc tcc				880
Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser				
255	260	265		
aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga cac tgc atc				928
Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile				
270	275	280		
tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg gtg ctt tca				976
Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser				
285	290	295		
gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg ctg ctg ctg				1024
Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu				
300	305	310	315	
gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg gtc acc acg				1072
Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr				
320	325	330		
gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc tcc gag gac				1120
Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp				
335	340	345		
350	355	360		

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gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc acc ttc ctg	1216
Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu	
365 370 375	
gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt cga gct ctg	1264
Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu	
380 385 390 395	
cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg agt ccc cat	1312
His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser Pro His	
400 405 410	
ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt gcc tac cag	1360
Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln	
415 420 425	
aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc atc ttc ttc	1408
Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe	
430 435 440	
ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct gtg ctc cat	1456
Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His	
445 450 455	
ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tgg tgg ccc ttc	1504
Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe	
460 465 470 475	
tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg gca gcc cat	1552
tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg acc aac cgg	1600

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Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg  
 495 500 505  
 cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc aat gtg ctg 1648  
 Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu  
 510 515 520  
 gtg ggt gcc atg gtg gcc acc tgg cga gtg ctc ctc tct gcc ctc tac 1696  
 Val Gly Ala Met Val Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr  
 525 530 535  
 aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg cca ccg aga 1744  
 Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg  
 540 545 550 555  
 gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac ttc ttg aag 1792  
 Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys  
 560 565 570  
 att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc tgc tcc ctg 1840  
 Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu  
 575 580 585  
 ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca gcc ccc cag 1888  
 Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln  
 590 595 600  
 gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag ctg cta cag 1936  
 Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln  
 Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly

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620	625	630	635	
agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac cca acc ctg				2032
Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu				
	640	645	650	
cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt gcc cag ccc				2080
Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro				
	655	660	665	
tgagggcagg gaaggtcaac ccacctgcc atctgtctg aggcattgtc				2130
ctgcctacca tctcctccc tccccggctc tctcccagc atcacaccag ccattgcagc				2190
agcaggctct ccggatcacc gtggttggtt ggaggtctgt ctgcactggg agcctcagga				2250
gggtctctgt ccacccactt ggctatggga gagccagcag gggttctgga gaaagaaact				2310
ggtgggttag ggccttggtc caggagccag ttgagccagg gcagccacat ccaggcgtct				2370
ccctaccctg gctctgccat cagccttgaa gggcctcgat gaagccttct ctggaaccac				2430
tccagcccag ctccacctca gccttggcct tcacgtgtg gaagcagcca aggcacttcc				2490
tcacccctc agcgccacgg acctctctgg ggagtggccg gaaagctccc gggcctctgg				2550
cctgcagggc agcccaagtc atgactcaga ccaggtecca cactgagctg cccacactcg				2610
agagccagat atttttgtag tttttatgcc tttggctatt atgaaagagg ttagtgtgtt				2670
ccctgcaata aacttggtcc tgag				2694

&lt;210&gt; 57

&lt;211&gt; 3297

&lt;212&gt; DNA

&lt;221&gt; CDS



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&lt;222&gt; (83)... (1477)

&lt;400&gt; 57

ggggtctgta ctctgtgaag tcaactgggt tagtgtgctc tctgatgcct ggaattccag 60

tccccacca gaaacccgca gc atg att gtc tgc ctc ctt ttc atg atg att 112

Met Ile Val Cys Leu Leu Phe Met Met Ile

1

5

10

tta ttg gca aag gaa gtt caa ctg gta gac caa aca gat tca cct tta 160

Leu Leu Ala Lys Glu Val Gln Leu Val Asp Gln Thr Asp Ser Pro Leu

15

20

25

ctt agt ctc ctt gga cag aca agc tca ctt tca tgg cat ctt gtg gat 208

Leu Ser Leu Leu Gly Gln Thr Ser Ser Leu Ser Trp His Leu Val Asp

30

35

40

att gtg tgc tac cag agt gtg cta agt tat ttc agc agc cat tac ccg 256

Ile Val Ser Tyr Gln Ser Val Leu Ser Tyr Phe Ser Ser His Tyr Pro

45

50

55

ccg tcc atc atc ctg gca aaa gaa tct tat gct gaa tta atc atg aag 304

Pro Ser Ile Ile Leu Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys

60

65

70

ctc cta aaa gtg tct gcg ggc ctt tct att cct act gac agc cag aag 352

Leu Leu Lys Val Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys

75

80

85

90

cat ctt gat gca gtt cca aaa tgc caa gct ttt act cat cag atg gtt 400

caa ttc ctc agc acc ctg gaa caa aat gga aaa atc acc tta gca gtc 448

123/307

Gln Phe Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val  
 110 115 120  
 cta gaa cag gaa atg tct aag ctc tta gac gat atc att gtc ttt aac 496  
 Leu Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn  
 125 130 135  
 ccg ccc gac atg gac agc cag acc cgc cac atg gcc ctc agc agc ctc 544  
 Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser Leu  
 140 145 150  
 ttt atg gaa gtc ctg atg atg atg aac aac gcg act att cca aca gca 592  
 Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro Thr Ala  
 155 160 165 170  
 gag ttc ctt cgg ggc agt atc cgg acc tgg att ggc caa aaa atg cat 640  
 Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln Lys Met His  
 175 180 185  
 ggg ctg gtg gtg ctg ccc ctt tta aca gca gcc tgc cag agc ctg ggc 688  
 Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala  
 190 195 200  
 tcc gtc cgc cac atg gct gag act aca gaa gcc tgc atc act gcc tac 736  
 Ser Val Arg His Met Ala Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr  
 205 210 215  
 ttc aaa gaa agc cct ctc aat cag aat tca gga tgg gga ccc att ctg 784  
 Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu  
 Val Ser Leu Gln Val Pro Glu Leu Thr Met Glu Glu Phe Leu Gln Glu

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235	240	245	250	
tgc ctc acc ttg ggc agt tac ttg act ctt tac gtc tac ttg ctt cag				880
Cys Leu Thr Leu Gly Ser Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln				
	255	260	265	
	tgt tta aac agc gaa cag act tta agg aat gaa atg aaa gtg ctg ctc			928
	Cys Leu Asn Ser Glu Gln Thr Leu Arg Asn Glu Met Lys Val Leu Leu			
	270	275	280	
	atc tta agc aag tgg ctg gaa cag gtg tac cca agc tcc gtg gag gaa			976
	Ile Leu Ser Lys Trp Leu Glu Gln Val Tyr Pro Ser Ser Val Glu Glu			
	285	290	295	
	gag gca aag ctg ttt ttg tgg tgg cac caa gtc ctt cag ctc tcc ctc			1024
	Glu Ala Lys Leu Phe Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu			
	300	305	310	
	att cag aca gag cag aat gac tcc gtc ctg aca gaa tct gtc att cga			1072
	Ile Gln Thr Glu Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg			
315	320	325	330	
	att ctg ctc ttg gtt cag agc agg cag aac ctc gtg gct gag gag aga			1120
	Ile Leu Leu Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg			
	335	340	345	
	ctc agc tct ggg atc ctg ggg gca att ggg ttt ggc cgg aag tcg cct			1168
	Leu Ser Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro			
	350	355	360	

365

370

375

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tca gtt cag gtt cct atg gaa gat cag atc cgt ttg agg cct ggc tct	1264
Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser	
380 385 390	
gaa tta cat ctg acc ccc aaa gct cag cag gct ctg aat gct ctt gaa	1312
Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu	
395 400 405 410	
tcc atg gca tca agt aag cag tat gtt gaa tac cag gat caa ata ttg	1360
Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu	
415 420 425	
caa gcc acc caa ttt ata agg cat cct ggc cat tgc ctt caa gat ggg	1408
Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys Leu Gln Asp Gly	
430 435 440	
aaa agc ttc ttg gct ctt ctc gtt aac tgt ctg tat cca gaa gtg cat	1456
Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu Tyr Pro Glu Val His	
445 450 455	
tat ttg gac cac ata cga tagtta acactgagge tcttgaaaaa cccattgctg	1510
Tyr Leu Asp His Ile Arg	
460	
tttatgttta catttaactt tgetgttgca caagtaactt tgetcaattg cactgtagag	1570
ctcagtttgg ccaatgtgta gttgactgag atgcaagttg ggaggcgtta gatattagat	1630
aattttgggg tgtgtgtgtg tgtgtgtgtg tgttttctta gctcttaaga ccttctgggg	1690
actctttaag tttttatatt tatccacaag agaaacttac taagtccac ttgggtgcag	1750
tcactcagta cccttacttt taaaccccat ttgtgttctt ccaaagtaaa gaagtcaatt	1930

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ttgaaaaatt tctgcatttc tcaaattgtg acaaatacaa tagttttaaa gtattgtttt 1990  
tctcagaagg gagataaaaa tgccgagtta gttaaagtgg gtcattgtga aaatacgacc 2050  
acttgatcgt gattatagtg ggcagtagag atgatgacaa gtcaatttcc atccagccgt 2110  
gtatcctcat ggagaagctg cctgtctgaa tcaggatggc aagctggcag tctgggagga 2170  
gcatgttttg cacagatgtt ttgtttggc cacttgggtga ggagtgcaga cagggtgcc 2230  
tctctctagt cgggagagtc tgtgcattcc ctggggccct gaccctagcc tcattcacat 2290  
cacttgcccc tgtcgacacc taagtttgca cctttgata gacaccatgt tcgatatctg 2350  
aaaggctcag tgtcaggaga cagagactga gggagactga agacctgatt ctctgttccc 2410  
tgcttgtttt ttaacttcaa actcagatga agccaatgga cctgctgaaa cacttgctctg 2470  
tggaaactgg gtcaggtcgg gagatctact gaaatttggc ttttttcca tagccacgtg 2530  
ccttctgttg ttgacagttc attcattacc aaagcctgtg tgtaactttg ccttgttctg 2590  
tggccatctt cttgctcatg ttatttctcc tgggaatgag cagtttgact tctgttccca 2650  
cgttcctcat tctatcagct ctagatggat ttgcctgca tagctggctt aatatgtctt 2710  
tgtgtatggg tagtctgtag cctgagaata ttacctaaa aatgtctaaa cagccaccaa 2770  
gaatgtttat aggggtatag gaatatagtt aacagagtgc taatctctcc tcaaattgtc 2830  
ttttggaatg cttcccccaa aattgggaag ttggtaggag cttttcttta ctttgaattt 2890  
ctttacttgg acagaacgat tctgccttaa agacacgctt tgcagctctg ataaagaaca 2950  
tccctgttta gtctcttgag ttttacaggc caaaaatgt ccgtctcaga gggatctgtc 3010  
tcagcttttc ttatttttgc ttctctccgt ttcaaaaatt aatcatcttg ttctctgtat 3070  
aagaaaattt gagaagctgt ggacaattta atagtctgat ctggcaacag cgatttttgt 3130  
ttggaaatat ttgtgtttt ctttgaggag gatataatta ctgatacctt aggatgtgaa 3190  
attttgagt gacagtatgc acattttaaa gaaaattatg attaactctgt ataattgttt 3250

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&lt;211&gt; 2126

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (61)... (1473)

&lt;400&gt; 58

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aacactgaca gcgtgagccc gcggcggctg ctgccatggt ggctggcggc cgggtgcagc      60
atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg      108
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
      1           5           10          15
ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc      156
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
           20           25           30
cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc      204
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
           35           40           45
aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg      252
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
           50           55           60
ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc      300
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

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85	90	95	
gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga			396
Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg			
100	105	110	
agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc			444
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys			
115	120	125	
cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt			492
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe			
130	135	140	
gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg			540
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr			
145	150	155	160
gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac			588
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr			
165	170	175	
aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa			636
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu			
180	185	190	
agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg			684
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly			
195	200	205	
210	215	220	

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agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc	780
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro	
225                      230                      235                      240	
ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag	828
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys	
245                      250                      255	
cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc	876
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser	
260                      265                      270	
cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt	924
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys	
275                      280                      285	
gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga	972
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly	
290                      295                      300	
aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac	1020
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp	
305                      310                      315                      320	
tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag	1068
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu	
325                      330                      335	
agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg	1116
gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt	1164



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Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu  
 355 360 365  
 ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa 1212  
 Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys  
 370 375 380  
 aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa 1260  
 Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu  
 385 390 395 400  
 gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt 1308  
 Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe  
 405 410 415  
 tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg 1356  
 Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly  
 420 425 430  
 aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca 1404  
 Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro  
 435 440 445  
 gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg 1452  
 Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu  
 450 455 460  
 gaa gtc att tta cga gac taaccacgtt tcaactggcct tcatgacttg 1500  
 Glu Val Ile Leu Arg Asp  
 gaaaccaca caaatctgtc tcttgggtct gactgctacc cactaccaact cccattagt 1620

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taattttattc taacctetaa cctaattctag aattggggca gtactcatgg ctcccgtttc 1680  
 tgttggttctc tcccttgagt aatctcttaa aaaaatcaag attcacacct gcccaggat 1740  
 tacacatggg tagagcctgc aagacctgag accttccaat tgctggtgag gtggatgaac 1800  
 ttcaaagcta taggaacaaa gcacataact tgtcacttta atctttttca ctgactaata 1860  
 ggactcagta catatagtct taagatcata ccttacctac caaggtaaaa agagggatca 1920  
 gagtggccca cagacattgc tttcttatca cctatcatgt gaattctacc tgtattcctg 1980  
 ggctggacca cttgataact tccagtgtcc tggcagcttt tggaatgaca gcagtggat 2040  
 ggggtttatg atgctataaa acaatgtctg aaaagttgcc tagaatatat tttgttacia 2100  
 acttgaaata aaccaaattt gatgtt 2126

&lt;210&gt; 59

&lt;211&gt; 1781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (74)... (805)

&lt;400&gt; 59

aatttggaac tgtgattcct tggttctcac aatcctctcc actctaagaa gcagggtgag 60  
 cccacaagga gca atg gag cag ggc agc ggc cgc ttg gag gac ttc cct 109

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro

1

5

10

15

20

25

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cag gtg tcc gat gat gac aag gcg ggg gcc acc ttg ctc ttc tca ggc	205
Gln Val Ser Asp Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly	
30 35 40	
atc ttt ctg gga ctg gtg ggg atc aca ttc act gtc atg ggc tgg atc	253
Ile Phe Leu Gly Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile	
45 50 55 60	
aaa tac caa ggt gtc tcc cac ttt gaa tgg acc cag ctc ctt ggg ccc	301
Lys Tyr Gln Gly Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro	
65 70 75	
gtc ctg ctg tca gtt ggg gtg aca ttc atc ctg att gct gtg tgc aag	349
Val Leu Leu Ser Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys	
80 85 90	
ttc aaa atg ctc tcc tgc cag ttg tgc aaa gaa agt gag gaa agg gtc	397
Phe Lys Met Leu Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val	
95 100 105	
ccg gac tcg gaa cag aca cca gga gga cca tca ttt gtt ttc act ggc	445
Pro Asp Ser Glu Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly	
110 115 120	
atc aac caa ccc atc acc ttc cat ggg gcc act gtg gtg cag tac atc	493
Ile Asn Gln Pro Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile	
125 130 135 140	
cct cct cct tat ggt tct cca gag cct atg ggg ata aat acc agc tac	541
ctg cag tct gtg gtg agc ccc tgc ggc ctc ata acc tct gga ggg gca	589

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Leu Gln Ser Val Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala  
 160 165 170  
 gca gcc gcc atg tca agt cct cct caa tac tac acc atc tac cct caa 637  
 Ala Ala Ala Met Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln  
 175 180 185  
 gat aac tct gca ttt gtg gtt gat gag ggc tgc ctt tct ttc acg gac 685  
 Asp Asn Ser Ala Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp  
 190 195 200  
 ggt gga aat cac agg ccc aat cct gat gtt gac cag cta gaa gag aca 733  
 Gly Gly Asn His Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr  
 205 210 215 220  
 cag ctg gaa gag gag gcc tgt gcc tgc ttc tct cct ccc cct tat gaa 781  
 Gln Leu Glu Glu Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu  
 225 230 235  
 gaa ata tac tct ctc cct cgc tagagget attctgatat aataacacaa 830  
 Glu Ile Tyr Ser Leu Pro Arg  
 240  
 tgctcagctc agggagcaag tgtttccgctc attgttacct gacaaccgtg gtgttctatg 890  
 ttgtaacctt cagaagttac agcagcgccc aggcagcctg acagagatca ttcaaggggg 950  
 gaaaggggaa gtgggaggtg caatttctca gattggtaaa aattaggetg ggctggggaa 1010  
 attctctccc ggaacagttt caaattccct cgggtaagaa atctcctgta taaggttcag 1070  
 gagcaggaat ttcaactttt catccaccac cctccccctt ctctgtagga aggcattggt 1130  
 gatttcttgg tggtgtcctt tggccccaaa gcagactcac taatcccaaa caactcagct 1310

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gccatctggc ctctctgagg actctgggta ccttaaagac tataaaacaa aacaaaacaa 1370  
 aaacatcaaa ccaatgaaat aaaataaatc atgtctcctg ctagaatagt attggatacc 1430  
 tgactaaatt acacaaaata gaccataata ggatagcact gtgaatacat ccttcccgat 1490  
 cactgagtca cagtgaccct tggtctctgc agttctctgc tgcaagggtg aagcttgacg 1550  
 tgtgatgaac atgggtgggc tcttggtcca cccagcgtg gggcctgcgc caagcatgaa 1610  
 ctagctggga ccagtggctg acagaacaca ggacttcct aagtaccgt aggtccgtgg 1670  
 agcaagacag agcagagttg ccatgtcaac acatggggaa tgatatgata gaaacaatct 1730  
 ttatgactaa aagaaactca tcttcttcat taaaaaact ttggtgcct t 1781

&lt;210&gt; 60

&lt;211&gt; 1788

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)... (899)

&lt;400&gt; 60

attgggcggc gtgatctgc cgcggttcgc cggccctgcc gccgccgcc ccagcagagc 60  
 gcaccgggcc gatcgggcca gtggcc atg gcg ggc gcc gag gac tgg ccg ggc 113

Met Ala Gly Ala Glu Asp Trp Pro Gly

1

5

cag cag ctg gag ctg gac gag gac gag gcg tct tgt tgc cgc tgg ggc 161

gcg cag cac gcc ggg gcc cgc gag ctg gct gcg etc tac teg cca ggc 209

135/307

Ala Gln His Ala Gly Ala Arg Glu Leu Ala Ala Leu Tyr Ser Pro Gly  
 30 35 40  
 aag cgc ctc cag gag tgg tgc tct gtg atc ctg tgc ttc agc ctc atc 257  
 Lys Arg Leu Gln Glu Trp Cys Ser Val Ile Leu Cys Phe Ser Leu Ile  
 45 50 55  
 gcc cac aac ctg gtc cat ctc ctg ctg ctg gcc cgc tgg gag gac aca 305  
 Ala His Asn Leu Val His Leu Leu Leu Leu Ala Arg Trp Glu Asp Thr  
 60 65 70  
 ccc ctc gtc ata ctc ggt gtt gtt gca ggg gct ctc att gct gac ttc 353  
 Pro Leu Val Ile Leu Gly Val Val Ala Gly Ala Leu Ile Ala Asp Phe  
 75 80 85  
 ttg tct ggc ctg gta cac tgg ggt gct gac aca tgg ggc tct gtg gag 401  
 Leu Ser Gly Leu Val His Trp Gly Ala Asp Thr Trp Gly Ser Val Glu  
 90 95 100 105  
 ctg ccc att gtg ggg aag gct ttc atc cga ccc ttc cgg gag cac cac 449  
 Leu Pro Ile Val Gly Lys Ala Phe Ile Arg Pro Phe Arg Glu His His  
 110 115 120  
 att gac cca aca gct atc aca cgg cac gac ttc atc gag acc aac ggg 497  
 Ile Asp Pro Thr Ala Ile Thr Arg His Asp Phe Ile Glu Thr Asn Gly  
 125 130 135  
 gac aac tgc ctg gtg aca ctg ctg cgg ctg cta aac atg gcc tac aag 545  
 Asp Asn Cys Leu Val Thr Leu Leu Pro Leu Leu Asn Met Ala Tyr Lys  
 Phe Arg Thr His Ser Pro Glu Ala Leu Glu Gln Leu Tyr Pro Trp Glu

136/307

155	160	165	
tgc ttc gtc ttc tgc ctg atc atc ttc ggc acc ttc acc aac cag atc			641
Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe Thr Asn Gln Ile			
170	175	180	185
cac aag tgg tgc cac acg tac ttt ggg ctg cca cgc tgg gtc acc ctc			689
His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg Trp Val Thr Leu			
	190	195	200
ctg cag gac tgg cat gtc atc ctg cca cgt aaa cac cat cgc atc cac			737
Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His His Arg Ile His			
	205	210	215
cac gtc tca ccc cac gag acc tac ttc tgc atc acc aca ggc tgg ctc			785
His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr Thr Gly Trp Leu			
	220	225	230
aac tac cct ctg gag aag ata ggc ttc tgg cga cgc ctg gag gac ctc			833
Asn Tyr Pro Leu Glu Lys Ile Gly Phe Trp Arg Arg Leu Glu Asp Leu			
	235	240	245
atc cag ggc ctg acg ggc gag aag cct cgg gca gat gac atg aaa tgg			881
Ile Gln Gly Leu Thr Gly Glu Lys Pro Arg Ala Asp Asp Met Lys Trp			
250	255	260	265
gcc cag aag atc aaa taac ttctccgagc ctgctacctg gttgcccaacc			930
Ala Gln Lys Ile Lys			
	270		
agaataacttg agccactgat ttttcatttc tttttttttt tttttctcg gccctctctc			
			1110

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agccacctga gttgctctat ctgcaagect gactctgcca gcctcccttg gtagagagga 1170  
 ggtttaccca ctccctgcac gcctgccgtc cctgccccgc tgggcagccc ttcagtgtgg 1230  
 ctggcggttg ggccagttag ttgcctcttt cctccttgt ctggccccag tggctctgggg 1290  
 agccccagg cacacctaag cgtcgtggag cattgttctg ccacagccct gcatactgac 1350  
 cccgggaggg tgggcaggtg gacagcccca gccaccacct tcagcctagc ctgtcccca 1410  
 aggatggtga agctcagcag gggctctgagg gtagccggcc agaagaggct ggaacctcct 1470  
 gctcaagtct agaccctac ttctctgctg cccccacct gccagagctg atgtttccaa 1530  
 taccaagatg tcttcacagg gcacagcccc tgcagagcat cttggtcatt tggaagagga 1590  
 cacggtatcc cctctggcca gagtatgtca gagaaggaag agtagggctt tttgttttg 1650  
 ttttttttta aagggtcttg cttgtttaat gtaaataata gaaagcetta atatcttttc 1710  
 tgtaacacgg agtaatattt taatgtcatg ttttgatgt acataatata ttataacaa 1770  
 agcagcaaga gtctactt 1788

&lt;210&gt; 61

&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

Met Asp Arg Gly Glu Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp

1

5

10

15

Trp Gly Thr Ser Phe Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe

20

25

30

Ser Leu Cys Val Trp Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr



138/307

50	55	60	
Leu Cys Ser Ala Glu Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln			
65	70	75	80
Tyr Tyr Phe Leu Lys Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn			
85	90	95	
Leu Trp Thr Ser Leu Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala			
100	105	110	
Leu Leu Leu Ala Glu Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser			
115	120	125	
Val Pro Lys Leu Pro Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile			
130	135	140	
Val Gly Ile Leu Thr Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln			
145	150	155	160
Ile Ala Ser Ser Val Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu			
165	170	175	
Thr Gly Val Val Phe Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg			
180	185	190	
Phe Gln Asn Ala Phe Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile			
195	200	205	
Gln Ala Ile Phe Gln Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys			
210	215	220	
Pro Arg Thr Thr Ile Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val			

245

250

255

139/307

Pro Arg Glu Ile Leu Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp

260

265

270

Arg Ala Phe Pro Ser Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr

275

280

285

Ser Leu Phe Ser Asn Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro

290

295

300

Ile Tyr Leu Ala Ser Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr

305

310

315

320

Leu Asn Ser His Ser Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr

325

330

335

Leu Gly Ser Leu Ala Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn

340

345

350

Tyr Ile Phe Phe Thr Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly

355

360

365

Ile Leu Arg Arg Arg Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys

370

375

380

Val Lys Leu Asp Phe

385

&lt;210&gt; 62

&lt;211&gt; 348

&lt;212&gt; PRT

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

140/307

1	5	10	15												
Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	Leu	Leu
	20		25		30										
Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	Gln	Thr	Phe
	35		40		45										
Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	Tyr	Gln	Gly	Val
	50		55		60										
Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	Gly	Asn	Ala	Met	Val
	65		70		75									80	
Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	Met	Gln	Ser	Lys	Gln	Gly
		85			90									95	
Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	Leu	Arg	Asp	Trp	Glu	Leu	Gln
	100		105		110										
Val	His	Phe	Lys	Ile	His	Gly	Gln	Gly	Lys	Lys	Asn	Leu	His	Gly	Asp
	115		120		125										
Gly	Leu	Ala	Ile	Trp	Tyr	Thr	Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val
	130		135		140										
Phe	Gly	Asn	Met	Asp	Lys	Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr
	145		150		155									160	
Tyr	Pro	Asn	Glu	Glu	Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser
		165			170									175	
Ala	Met	Val	Asn	Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly

195

200

205

141/307

Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile

210

215

220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val

225

230

235

240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile

245

250

255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe

260

265

270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp

275

280

285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala

290

295

300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe

305

310

315

320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr

325

330

335

Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr

340

345

&lt;210&gt; 63

&lt;211&gt; 261

&lt;212&gt; PRT

Page 4

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys

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1	5	10	15
Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val			
20	25	30	
Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu			
35	40	45	
Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr			
50	55	60	
Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe			
65	70	75	80
Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg			
85	90	95	
Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu			
100	105	110	
Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr			
115	120	125	
Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro			
130	135	140	
Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr			
145	150	155	160
Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly			
165	170	175	
Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile			

195

200

205

143/307

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro

210

215

220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu

225

230

235

240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln

245

250

255

Gly Lys Thr Lys Asn

260

&lt;210&gt; 64

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu

1

5

10

15

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg

20

25

30

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr

35

40

45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg

50

55

60

Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu

144/307

85	90	95	
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile			
100	105	110	
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile			
115	120	125	
Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile Trp Ile			
130	135	140	
Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile Ala Leu			
145	150	155	160
Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro			
165	170	175	
Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile			
180	185	190	
Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly His Ile			
195	200	205	
Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu			
210	215	220	

&lt;210&gt; 65

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

1 5 10 15

145/307

Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys Gly Asn Pro Glu

20

25

30

His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr Ile Trp Leu Leu

35

40

45

Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu Thr Ser Leu Cys

50

55

60

Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly Glu Asp Gly Gly

65

70

75

80

Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp His Asp Ser Thr

85

90

95

Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe Gly Pro Ala Ala

100

105

110

Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser Leu Gly Gln Leu

115

120

125

Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu Ala Leu His Met

130

135

140

Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala Pro Asp Leu Pro

145

150

155

160

Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu Lys Glu Ser Thr

165

170

175

Arg Ile Val Asp Ser Trp Asn

180

&lt;211&gt; 262



146/307

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Met Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn

1 5 10 15

Lys Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn

20 25 30

Tyr Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys

35 40 45

Glu Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly

50 55 60

Ser Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile

65 70 75 80

Pro Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val

85 90 95

Phe Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe

100 105 110

Phe Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser

115 120 125

Ser Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn

130 135 140

Ile Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln

165

170

175

147/307

Asn Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe

180

185

190

Tyr Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys

195

200

205

Thr Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly

210

215

220

Thr Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln

225

230

235

240

Ser Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln

245

250

255

Leu Thr Pro His Pro Pro

260

&lt;210&gt; 67

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser

1

5

10

15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro

20

25

30

Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys

148/307

50                      55                      60  
 Leu Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser  
 65                      70                      75                      80  
 Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly  
                     85                      90                      95  
 Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro  
                     100                      105                      110  
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro  
                     115                      120                      125  
 Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser  
                     130                      135                      140  
 Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro  
 145                      150                      155                      160  
 Asp Ser Pro Asn Phe Glu Val Ile  
                     165

&lt;210&gt; 68

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val

149/307

Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp  
35 40 45  
Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala  
50 55 60  
Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu  
65 70 75 80  
Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln  
85 90 95  
Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp  
100 105 110  
Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro  
115 120 125  
Glu Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln  
130 135 140  
Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys  
145 150 155 160  
Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser  
165 170 175  
Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp  
180 185 190  
Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val  
195 200 205  
Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala

150/307

225 230 235 240

Thr Glu Ala

&lt;210&gt; 69

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

Met Ala Arg Ser Leu Cys Pro Gly Ala Trp Leu Arg Lys Pro Tyr Tyr

1 5 10 15

Leu Gln Ala Arg Phe Ser Tyr Val Arg Met Lys Tyr Leu Phe Phe Ser

20 25 30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser

35 40 45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys

50 55 60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu

65 70 75 80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Thr Lys Pro

85 90 95

Asn Asn Gln Met Tyr Leu Gly Ile Trp Asp Asn Leu Pro Gly Val Val

115

120

125

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Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr

130

135

140

Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys

145

150

155

160

Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr

165

170

175

Val Ala Asp Gly Asp Lys Asp Gly Gln Val Ser Leu Gly Glu Ala Lys

180

185

190

Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile

195

200

205

Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp

210

215

220

Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser

225

230

235

240

Leu Pro Trp Val Ile Glu Leu Phe Ile Pro Ser Gly Phe Arg Arg Ser

245

250

255

Met Asp Gln Leu Phe Thr Pro Ser Trp Pro Arg Lys Ala Lys Ile Ala

260

265

270

Ile Gly Leu Leu Glu Phe Val Glu Asp Val Phe His Gly Pro Tyr Gly

275

280

285

Asn Phe Leu Met Cys Asp Thr Ser Ala Lys Asn Leu Gly Tyr Asn Asp

290

295

300

Asn Leu Lys Glu Leu Ile Lys Asp Arg His Cys Glu Ser Asp Leu Asp

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325 330 335  
Cys Val Tyr Gly Thr Asp Cys Arg Thr Ser Cys Asp Gln Ser Thr Met  
340 345 350  
Lys Cys Thr Ser Glu Val Ile Gln Pro Asn Leu Ala Lys Ala Cys Gln  
355 360 365  
Leu Leu Lys Asp Tyr Leu Leu Arg Gly Ala Pro Ser Glu Ile Arg Glu  
370 375 380  
Glu Leu Glu Lys Gln Leu Tyr Ser Cys Ile Ala Leu Lys Val Thr Ala  
385 390 395 400  
Asn Gln Met Glu Met Glu His Ser Leu Ile Leu Asn Asn Leu Lys Thr  
405 410 415  
Leu Leu Trp Lys Lys Ile Ser Tyr Thr Asn Asp Ser  
420 425

&lt;210&gt; 70

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His

1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr

Seq. 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Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys

50

55

60

Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser

65

70

75

80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly

85

90

95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

100

105

110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln

115

120

125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

130

135

140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala

145

150

155

160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

165

170

175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly

180

185

190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

195

200

205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

210

215

220

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln



154/307

245	250	255
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Arg Arg Lys Arg Lys Arg Leu Leu Trp Ala Ala		
275	280	

&lt;210&gt; 71

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

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155/307

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&lt;210&gt; 72

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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156/307

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&lt;210&gt; 73

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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aac

783

157/307

&lt;210&gt; 74

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

atgtttgtggc tgctcttttt tctgggtgact gccattcatg ctgaactctg tcaaccaggt	60
gcagaaaatg cttttaaaagt gagacttagt atcagaacag ctctgggaga taaagcatat	120
gcctgggata ccaatgaaga atacctcttc aaagcgatgg tagctttctc catgagaaaa	180
gttcccaaca gagaagcaac agaaatttcc catgtcctac ttgcaatgt aaccagagg	240
gtatcattct ggtttgtggt tacagaccct tcaaaaaatc acacccttcc tgctgttgag	300
gtgcaatcag ccataagaat gaacaagaac cggatcaaca atgccttctt tctaaatgac	360
caaactctgg aatttttaaa aatcccttcc acacttgac caccatgga cccatctgtg	420
cccatctgga ttattatatt tgggtgtgata ttttgcata tcatagtgc aattgacta	480
ctgattttat cagggatctg gcaacgtaga agaaagaaca aagaaccatc tgaagtggat	540
gacgctgaag ataagtgtga aaacatgac acaattgaaa atggcatccc ctctgatccc	600
ctggacatga agggagggca tattaatgat gccttcatga cagaggatga gaggtcacc	660
cctctc	666

&lt;210&gt; 75

&lt;211&gt; 549

&lt;212&gt; DNA

atgggagtc gagttcatgt cgtggggccc tcagccctgc tgtatttcat cctgctttct	60
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158/307

gggacgagat gtgaggaaaa ctgttgtaat cctgaacatt gcctgaccac agactgggta 120  
 catctctggt atatatgggt gctagtggta attggcgcgc tgcttctcct gtgtggcctg 180  
 acgtccctgt gcttccgctg ctgctgtctg agccgccagc aaaatgggga agatgggggc 240  
 ccaccaccct gtgaagtgac cgtcattgct ttgatcacg acagcactct ccagagcact 300  
 atcacatctc tgcagtcggt gtttggccct gcagctcgga ggatcctggc tgtggctcac 360  
 tcccacagct ccttgggcca gctgccctcc tctttggaca cctcccagg gtatgaagaa 420  
 gctcttcaca tgagtcgctt cacagtagcc atgtgcgggc agaaagcacc tgatctacce 480  
 ccagtaacctg aagaaaagca gctgcctcca acagagaagg agtcgactcg aatagttgac 540  
 tcttggaac 549

&lt;210&gt; 76

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

atgggtaaga cgttttccca gctgggctct tggcgggagg atgagaacaa gtcaatcctg 60  
 tcttccaaac cagccattgg cagcaaggct gtcaactact ccagcaccgg tagcagcaag 120  
 tctttttgtt cctgtgtgcc ttgtgaagga actgctgatg ccagcttcgt gacttgtccc 180  
 acctgccagg gcagtggcaa gattcccca gagctggaga agcagttggt ggetctcatt 240  
 ccctatgggg accagaggct gaagcccaag cacacgaagc tctttgtgtt cctggccgtg 300  
 ctcatctgcc tggtagacct ctccttcacg gtctttttcc tgtttccccg gtccgtcatt 360  
 gtgcagcctg caggccctca ctcctccaca gtggcctttg atgaggetga tatctacctc 420

tgcctctg ccttttctga - tctctt ttttttctga ccttttctga ccttttctga

ctacacattg gccctttggc cagtgaacag atgttttacg cagtagctac caagatacgg 600

159/307

gatgaaaaca catacaaaaat ctgtacctgg ctggaaatca aagtcacca tgtgtctttg 660  
 cacatccagg gcacctgac ctgttcatac ctgagccatt cagagcagct ggtctttcag 720  
 agctatgaat atgtggactg ccgaggaaac gcatctgtgc cccaccagct gacctctcac 780  
 ccacca 786

&lt;210&gt; 77

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

atgggcgtcc ccacggccct ggaggccggc agctggcgct ggggatacct gctcttcgct 60  
 ctcttctctgg ctgcgtccct aggcaaagat gcaccatcca actgtgtggt gtacccatcc 120  
 tctctccagg agagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 180  
 ggaatcctct gcctccccct catctgctc ctggtctaca agcaaaggca ggcagcctcc 240  
 aaccgcctg cccaggagct ggtgcggatg gacagcaaca ttcaagggat tgaaaacccc 300  
 ggctttgaag cctcaccacc tgcccagggg ataccgagg ccaaagtcag gcacccctg 360  
 tctatgtgg cccagcggca gccttctgag tctggcggc atctgcttcc ggagcccagc 420  
 accccctgt ctctccagg ccccgagac gtcttcttcc catccctgga cctgtcct 480  
 gactctecaa actttgaggt catc 504

&lt;210&gt; 78

&lt;211&gt; 729

&lt;212&gt; Homo sapiens

&lt;400&gt; 78

160/307

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atgagctcgg ggactgaact gctgtggccc ggagcagcgc tgctgggtgct gttgggggtg      60
gcagccagtc tgtgtgtgcg ctgctcacgc ccagggtcaa agaggtcaga gaaaatctac      120
cagcagagaa gtctgcgtga ggaccaacag agctttacgg ggtcccggac ctactccttg      180
gtcgggcagg catggccagg acccctggcg gacatggcac ccacaaggaa ggacaagctg      240
ttgcaattct accccagcct ggaggatcca gcattctcca ggtaccagaa cttcagcaaa      300
ggaagcagac acgggtcggg ggaagcctac atagaccca ttgccatgga gtattacaac      360
tgggggcggg tctcgaagcc ccagaagat gatgatgcca attcctacga gaatgtgctc      420
atttgcaagc agaaaaccac agagacaggt gccagcagg agggcatagg tggcctctgc      480
agaggggacc tcagcctgtc actggccctg aagactggcc ccacttctgg tctctgtccc      540
tctgcctccc cggaagaaga tgaggaatct gaggattatc agaactcagc atccatccat      600
cagtggcgcg agtcaggaa ggtcatgggg caactccaga gagaagcatc ccctggcccc      660
gtgggaagcc cagacgagga ggacggggaa ccgattacg tgaatgggga ggtggcagcc      720
acagaagcc                                         729

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&lt;210&gt; 79

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

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atggcgagga gtctctgtcc gggggcctgg ctaaggaaac cctattacct ccaggtcgc      60
ttctcatatg tgcggatgaa atatcttttc ttttcttgt tagtggtttt tgttgaagc      120
tggattatat atgtgcagta ttctacctat acagaattat gcagaggaaa ggactgtaag      180
tatttaggga tttaggataa tetaccaggt gttgtgaaat gtcaaatgga acaagcgctt      360

```

161/307

catcttgatt ttggaactga attggaacca agaaaagaaa tagtgctatt tgataagcca 420  
actagaggaa ctactgtaca aaaatttaaa gaaatgggtct atagtctctt taaggcaaaa 480  
ttgggtgacc aaggaaacct ctctgaactg gttaatctca tcttgacggt ggctgatgga 540  
gacaaagatg gccaggtttc cttgggagaa gcaaagtcgg catgggcact tcttcaactg 600  
aatgaatttc ttctcatggt gatacttcaa gataaagaac ataccccca attaatggga 660  
ttctgtggtg acctctatgt gatgaaagt gtigaatata cctctcttta tggaataagc 720  
cttccctggg tcattgaact ttttattcca tctgggttca gaagaagcat ggatcagctg 780  
ttcacaccat catggccaag aaaggccaaa atagccatag gacttctaga atttgtggaa 840  
gatgttttcc atggccccta cggaaatttc ctcatgtgcg atactagtgc caaaaaccta 900  
ggatataatg ataagtatga ttgaaaatg gtggatatga gaaaaattgt gccagagaca 960  
aacctgaaag aacttattaa ggatcgtcac tgtgagtctg atttggactg tgtctatggc 1020  
acagattgta gaactagctg tgatcagagt acaatgaagt gtacttcaga agtgatacaa 1080  
ccaaacttgg caaaagcttg tcagttactc aaagactacc tactgcgtgg tgcctcaagt 1140  
gaaattcgtg aagaattaga aaagcagctt tattcttgta ttgctctcaa agtcacagca 1200  
aatcaaattg aaatggaaca ttctttgata ctaaataacc taaaaacatt attgtggaag 1260  
aaaatttcct acactaatga ctct 1284

&lt;210&gt; 80

&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

... .. 60  
gagcacactc tccggtacct gggtctccac ctagcctccc tgcagctggg actgctgtta 180



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aacggggtct gcagcctggc tgaggagctg caccacatcc actccaggta ccggggcagc 240  
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg 300  
ctgtccatct atttctacta ctccctccca aatgcggtcg gccgcctt cacttggatg 360  
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc 420  
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca 480  
tggtcatatt acatcgata tctgcggtg atcctgccag agctccaggc ccggattcga 540  
acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt 600  
ctctcccat tggactgtgg ggtgcctgat aacctgagta tggtgaccc caacattcgc 660  
ttcctggata aactgcccc aagacacgt gaccgtgctg gcatcaagga tcgggtttac 720  
agcaacagca tctatgagct tctggagaac gggcagcgga acctgcagat gacagcagct 780  
tctcgtgtc ccaggagggt ctccggcacc tgcggcagga ggaaaaggaa gaggttactg 840  
tgggcagct 849

&lt;210&gt; 81

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (100)... (1269)

&lt;400&gt; 81

atTTTTattt caggaatcca tcaacatcct ttgcagctac ataggcagga aaatctagaa 60

114

163/307

aaa ata cag ctc aag aga gtg ttt gga tat tgg tgg ggc aca agt ttt	162
Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp Trp Gly Thr Ser Phe	
10 15 20	
ttg ctt att aat atc att ggt gca gga att ttt gtg tcc ccc aaa ggt	210
Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe Val Ser Pro Lys Gly	
25 30 35	
gtg ttg gca tac tct tgc atg aac gtg gga gtc tcc ctg tgc gtt tgg	258
Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val Ser Leu Cys Val Trp	
40 45 50	
gct ggc tgt gcc ata ctg gcc atg aca tca act ctt tgc tct gca gag	306
Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr Leu Cys Ser Ala Glu	
55 60 65	
ata agt ata agc ttc cca tgc agt gga gct caa tac tat ttt ctc aag	354
Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln Tyr Tyr Phe Leu Lys	
70 75 80 85	
aga tac ttt ggc tcc acg gtt gct ttt ttg aat ctc tgg aca tcc ttg	402
Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn Leu Trp Thr Ser Leu	
90 95 100	
ttt ctg ggg tca ggg gta gtt gct ggc caa gct ctg ctc ctt gct gag	450
Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala Leu Leu Leu Ala Glu	
105 110 115	
tac agc atc cag cct ttt ttt ccc agc tgc tct gtc cca aag ctg cct	498
Val Phe Leu Leu Phe	
aag aaa tgt ctg gca ttg gcc atg ttg tgg att gta gga att ctg act	546

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Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile Val Gly Ile Leu Thr  
 135 140 145  
 tct cgt ggt gtg aaa gaa gtg act tgg ctt cag ata gct agc tca gtg 594  
 Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln Ile Ala Ser Ser Val  
 150 155 160 165  
 ctg aaa gtg tcc ata ctt agc ttc att tcc cta act gga gta gtg ttc 642  
 Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu Thr Gly Val Val Phe  
 170 175 180  
 ctg ata aga ggg aaa aag gag aat gta gaa cga ttt cag aat gct ttt 690  
 Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg Phe Gln Asn Ala Phe  
 185 190 195  
 gat gct gaa ctt cca gat atc tct cac ctt ata caa gcc atc ttc caa 738  
 Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile Gln Ala Ile Phe Gln  
 200 205 210  
 gga tat ttt gca tat tca ggg gag ctg aag aag ccc aga aca aca att 786  
 Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys Pro Arg Thr Thr Ile  
 215 220 225  
 ccc aaa tgc ata ttt act gcg tta cct ctg gtg act gta gtt tat tta 834  
 Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val Thr Val Val Tyr Leu  
 230 235 240 245  
 ctg gtt aac att tcc tat ctg act gtt ctg aca ccc agg gaa att ctc 882  
 Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr Pro Arg Glu Ile Leu  
 Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp Arg Ala Phe Pro Ser

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265	270	275	
tta gca tgg att atg cct ttt gct att tct acc tca tta ttt agc aac			978
Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr Ser Leu Phe Ser Asn			
280	285	290	
ctt ctg att tct ata ttt aaa tct tcg aga cca ata tat ctt gca agc			1026
Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro Ile Tyr Leu Ala Ser			
295	300	305	
caa gag ggc cag ctg cct ttg cta ttt aat aca ctt aat agt cac tct			1074
Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr Leu Asn Ser His Ser			
310	315	320	325
tct cca ttt aca gct gtg cta cta ctt gtc act ttg gga tcc ctt gca			1122
Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr Leu Gly Ser Leu Ala			
330	335	340	
att atc tta aca agt cta att gat ttg ata aac tat att ttt ttc acg			1170
Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn Tyr Ile Phe Phe Thr			
345	350	355	
ggg tca tta tgg tct ata tta tta atg ata gga ata cta agg cgg aga			1218
Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly Ile Leu Arg Arg Arg			
360	365	370	
tac cag gaa ccc aat cta tct ata cct tat aag gta aaa ttg gat ttc			1266
Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys Val Lys Leu Asp Phe			
375	380	385	
			1320

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&lt;210&gt; 82

&lt;211&gt; 2392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (22)... (1068)

&lt;400&gt; 82

gaagggtcgt tggtagggaaa g atg gcg gcg act ctg gga ccc ctt ggg tcg 51

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser

1

5

10

tgg cag cag tgg cgg cga tgt ttg tcg gct cgg gat ggg tcc agg atg 99

Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met

15

20

25

tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa gtc 147

Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val

30

35

40

ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg tcg 195

Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser

45

50

55

aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat ctg 243

Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu

Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp

167/307

75	80	85	90
atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc ctg			339
Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe Leu			
95	100	105	
aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga aag			387
Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys			
110	115	120	
aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg			435
Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg			
125	130	135	
atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg			483
Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu			
140	145	150	
gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag cgg			531
Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg			
155	160	165	170
gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat			579
Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr			
175	180	185	
gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc			627
Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala			
190	195	200	
205	210	215	

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aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag tgg 723  
 Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp  
 220 225 230  
 agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac 771  
 Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Glu Tyr Tyr  
 235 240 245 250  
 ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc 819  
 Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val  
 255 260 265  
 att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag 867  
 Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu  
 270 275 280  
 gaa aag ctc cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag 915  
 Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys  
 285 290 295  
 ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc 963  
 Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu  
 300 305 310  
 ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc 1011  
 Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
 315 320 325 330  
 att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc 1059  
 Ile Glu Ile Ile Ile Thr Ala Ile Thr Glu Glu Glu Glu Ala Ile Ile  
 ttc tac tgagc cctcctgctg ccaccacttt tgtgactgtc acccatgagg 1110

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Phe Tyr

tatggaagga gcaggcactg gcctgagcat gcagcctgga gagggttctt gtctctagea 1170  
 gctgggttggg gactatattc tgtcactgga gttttgaatg cagggaacccc gcattcccat 1230  
 ggttgtgcat ggggacatct aactctggtc tgggaagcca cccaccccag ggcaatgctg 1290  
 ctgtgatgtg cttttccctg cagtccttcc atgtgggagc agaggtgtga agagaattta 1350  
 cgtgggttgtg atgccaaaat cacagaacag aatttcatag cccaggctgc cgtgttgttt 1410  
 gactcagaag gcccttctac ttcagttttg aatccacaaa gaattaaaaa ctggtaacac 1470  
 cacaggcttt ctgaccatcc attcgttggg ttttgcaatt gacccaaccc tctgcctacc 1530  
 tgaggagctt tctttggaaa ccaggatgga aacttcttcc ctgccttacc ttcctttcac 1590  
 tccattcatt gtctctctg tgtgcaacct gagctgggaa aggcatttgg atgcctctct 1650  
 gttggggcct ggggctgcag aacacacctg cgtttcactg gccttcatta ggtggcccta 1710  
 gggagatggc tttctgcttt ggatcactgt tccctagcat gggctcttggg tctattggca 1770  
 tgtccatggc cttcccaatc aagtctcttc aggcctcag tgaagtttgg ctaaaggttg 1830  
 gtgtaaaaat caagagaagc ctggaagaca tcatggatgc catggattag ctgtgcaact 1890  
 gaccagctcc aggtttgatc aaacaaaag caacatttgt catgttgtct gaccatgtgg 1950  
 agatgtttct ggacttgcta gagcctgctt agctgcatgt tttgtagtta cgatttttgg 2010  
 aatcccactt tgagtgtga aagtgtagg aagctttctt ctacacctt gggcttgat 2070  
 attgcccaga gaagaaattt ggcttttttt ttcttaatgg acaagagaca gttgctgttc 2130  
 tcatgttcca agtctgagag caacagacce tcatcatctg tgcttgaag agttcactgt 2190  
 cattgagcag cacagcctga gtgtggcct ctgtcaacce ttattccact gccttatttg 2250  
 acaaggggtt acatgtgtct caccttactg ccttgggatt aaatcagtta caggccagag 2310  
 tctccttggg gggcctggaa ctctgagtcc tctatgaac ctctgtagcc taaatgaaat 2370

2392



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&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)... (840)

&lt;400&gt; 83

attgtccctg cctgcttctg gagaaagaag atattgacac catctacggg cacc atg 57

Met

1

gaa ctg ctt caa gtg acc att ctt ttt ctt ctg ccc agt att tgc agc 105

Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser

5

10

15

agt aac agc aca ggt gtt tta gag gca gct aat aat tca ctt gtt gtt 153

Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val

20

25

30

act aca aca aaa cca tct ata aca aca cca aac aca gaa tca tta cag 201

Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln

35

40

45

aaa aat gtt gtc aca cca aca act gga aca act cct aaa gga aca atc 249

Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr Ile

50

55

60

65

70

75

80

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aca agt aaa gat gaa gga ttg aaa gcc aca acc act gat gtc agg aag	345
Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg Lys	
85 90 95	
aat gac tcc atc att tca aac gta aca gta aca agt gtt aca ctt cca	393
Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu Pro	
100 105 110	
aat gct gtt tca aca tta caa agt tcc aaa ccc aag act gaa act cag	441
Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr Gln	
115 120 125	
agt tca att aaa aca aca gaa ata cca ggt agt gtt cta caa cca gat	489
Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro Asp	
130 135 140 145	
gca tca cct tct aaa act ggt aca tta acc tca ata cca gtt aca att	537
Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr Ile	
150 155 160	
cca gaa aac acc tca cag tct caa gta ata ggc act gag ggt gga aaa	585
Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly Lys	
165 170 175	
aat gca agc act tca gca acc agc cgg tct tat tcc agt att att ttg	633
Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile Leu	
180 185 190	
ccg gtg gtt att gct ttg att gta ata aca ctt tca gta ttt gtt ctg	681
Val Val Val Val Val Val Val Val Val Val Val Val Val Val Val Val	
gtg ggt ttg tac cga atg tgc tgg aag gca gat ccg ggc aca cca gaa	729

172/307

Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro Glu  
 210 215 220 225  
 aat gga aat gat caa cct cag tct gat aaa gag agc gtg aag ctt ctt 777  
 Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu Leu  
 230 235 240  
 acc gtt aag aca att tct cat gag tct ggt gag cac tct gca caa gga 825  
 Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln Gly  
 245 250 255  
 aaa acc aag aac tga cagcttgagg aattctctcc acacctaggc aataattacg 880  
 Lys Thr Lys Asn  
 260  
 cttaatcttc agctttctatg caccaagcgt ggaaaaggag aaagtctctgc agaatcaatc 940  
 ccgacttcca tacctgctgc tggactgtac cagacgtctg tcccagtaaa gtgatgtcca 1000  
 gctgacatgc aataatttga tggaatcaaa aagaaccccg gggtctctct gttctctcac 1060  
 atttaaaaat tccattactc catttacagg agcgttctta ggaaaaggaa ttttaggagg 1120  
 agaatttgtg agcagtgaat ctgacagccc aggaggtggg ctgctgata ggcattgactt 1180  
 tccttaatgt ttaaagtttt ccgggccaag aatttttatc catgaagact ttctacttt 1240  
 tctcggtgtt cttatattac ctactgttag tatttattgt ttaccactat gttaatgcag 1300  
 ggaaaagttg cacgtgtatt attaaatatt aggtagaaat cataccatgc tactttgtac 1360  
 atataagtat ttattctctg ctttcgtgtt acttttaata aataactact gtactc 1416

&lt;210&gt; 84

1000  
 1000

&lt;213&gt; Homo sapiens

173/307

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)... (694)

&lt;400&gt; 84

gccttggtgtt ttccaccctg aaaga atg ttg tgg ctg ctc ttt ttt ctg gtg 52

Met Leu Trp Leu Leu Phe Phe Leu Val

1

5

act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat gct ttt 100

Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe

10

15

20

25

aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca tat gcc 148

Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala

30

35

40

tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct ttc tcc 196

Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser

45

50

55

atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat gtc cta 244

Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu

60

65

70

ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt aca gac 292

Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp

75

80

85

90

95

100

105

174/307

aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat gac caa	388
Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln	
110 115 120	
act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc atg gac	436
Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp	
125 130 135	
cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt tgc atc	484
Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile	
140 145 150	
atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg caa cgt	532
Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg	
155 160 165	
aga aga aag aac aaa gaa cca tct gaa gtg gat gac gct gaa gat aag	580
Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys	
170 175 180 185	
tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat ccc ctg	628
Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu	
190 195 200	
gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag gat gag	676
Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu	
205 210 215	
agg ctc acc cct ctc tgaagggt gttgttctgc ttctcaaga aattaaacat	730
ttgtttctgt gtgactgctg agcatcctga aataccaaga gcagatcata tattttgttt	790

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caccattctt cttttgtaat aaattttgaa tgtgcttgaa agtgaaaagc aatcaattat 850  
 acccaccaac accactgaaa tcataagcta ttcacgactc aaaatattct aaaatatttt 910  
 tctgacagta tagtgataa atgtggatcat gtggtatttg tagttattga ttttaagcatt 970  
 tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct aaggaaaaat 1030  
 aaattttcca gtggagaata catataatat ggtgtagaaa tcattgaaaa tggatccttt 1090  
 ttgacgatca cttatatcac tctgtatatg actaagtaaa caaaagttag aagtaattat 1150  
 tgtaaattgga tggataaaaa tggaattact catatacagg gtggaatttt atcctgttat 1210  
 cacaccaaca gttgattata tattttctga atatcagccc ctaataggac aattctattt 1270  
 gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa agtaataatc 1330  
 atctcttttt gattgtg 1347

&lt;210&gt; 85

&lt;211&gt; 2284

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (75)... (626)

&lt;400&gt; 85

aaaatggcac agagcatiga aaggaggcaa cggatgccca gtgcaagatt ctgaagaagc 60  
 aggaattcag cccg atg gga gtc cga gtt cat gtc gtg gcg gcc tca gcc 110

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala

10

Leu Leu Tyr Phe Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys

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15	20	25	
ggt aat cct gaa cat tgc ctg acc aca gac tgg gta cat ctc tgg tat			206
Gly Asn Pro Glu His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr			
30	35	40	
ata tgg ttg cta gtg gta att ggc gcg ctg ctt ctc ctg tgt ggc ctg			254
Ile Trp Leu Leu Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu			
45	50	55	60
acg tcc ctg tgc ttc cgc tgc tgc tgt ctg agc cgc cag caa aat ggg			302
Thr Ser Leu Cys Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly			
65	70	75	
gaa gat ggg ggc cca cca ccc tgt gaa gtg acc gtc att gct ttc gat			350
Glu Asp Gly Gly Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp			
80	85	90	
cac gac agc act ctc cag agc act atc aca tct ctg cag tcg gtg ttt			398
His Asp Ser Thr Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe			
95	100	105	
ggc cct gca gct cgg agg atc ctg gct gtg gct cac tcc cac agc tcc			446
Gly Pro Ala Ala Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser			
110	115	120	
ctg ggc cag ctg ccc tcc tct ttg gac acc ctc cca ggg tat gaa gaa			494
Leu Gly Gln Leu Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu			
125	130	135	140

Ala Val His Met Ser Arg Thr Thr Val Ala Met Cys His Met Tyr Met

177/307

cct gat cta ccc cca gta cct gaa gaa aag cag ctg cct cca aca gag 590

Pro Asp Leu Pro Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu

160

165

170

aag gag tcg act cga ata gtt gac tct tgg aac tgatgag agctgtcatt 640

Lys Glu Ser Thr Arg Ile Val Asp Ser Trp Asn

175

180

ttataaatag gaggaggatg atgtccagag tctgtgggaa aatggaacac atacttttct 700

aaccctcaga agttttaaga tggcatctaa caccatcatt ctatgggaaa gatggttctt 760

actcttcgtt cacaggcctt tatactctcc gatacagaat gctctaattg ggaactctaa 820

ttttgtatcc aatggccaaa atctgcaagt aatctctagc cacactgatt actactaaac 880

caggaaagca tcaaggtatc ttgaattcct ttaactattg agtgcataata gaattcctgt 940

accacatga tactgcaagt tgtgtctctc tctgtcagct aatccactgc ggtaactgg 1000

aaaagaaaga caacagtgtc agcacagcca tcgacattaa tgcactgaat gcatgcatct 1060

ttctctctga gacagcaatc gattttacac ogaatgacaa tgatcatctt agacagcaca 1120

acataccac tcggatatct aaaagctagg gatggcattg ctgatatggg caaagagaac 1180

acagtatagt atttaagtgc caaatatcag tctttcttct tctctgttcc taccctcag 1240

cagtatgaaa aactccatac tgtgcagtca cagttggatt aattcttcag ttctctcgca 1300

ctgcaaacac atatatgtgc gcacatgcat gtatacctgc accctgtttt aactctaaag 1360

gaatagtgtt gctttaactc ttctctgttt tgccctggacc acttaaagcc acaacacctc 1420

tatagtgaca cacgctagtc tctagtgggt gccctcactg ccacctagag gagccatggt 1480

ggaaaacaca ctctctcctt tgagcctatc tgcacatctc tcgagttctt ggagcaaaaa 1540

ctaaatgctg aactaagcct gggtgagatg ctcccatgg accatgccgc agcacagtgc 1600

ctaaatgctg aactaagcct gggtgagatg ctcccatgg accatgccgc agcacagtgc 1660

tttgagatgg agttttgctc ttgtagccca ggctgggatg caatggcatg gtctcagctc 1780



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actgtaacct ccacctcccg gattcaagca attcttctgc ctcagcttcc cgactagctg 1840  
ggattacagc tgccctgccac cgtgcccagc taatttttgt atttttagtg gagagggggt 1900  
ttcaccatgt tggccagtct ggtctagaac tcctgaagtc aggtgatccg cccaccttgg 1960  
cctcccaaag tgetggaatt agaggcctga cccctgctc ctggcctgaa atctttaaag 2020  
ccgttttttc cctaaaaaac gggaaataat aacacctcag aaggtttttg tgaagatcaa 2080  
agaagctaaa tatatgtggc atgatttgta aagtgttatg catatgtatg ttattcttcc 2140  
tactgtcttc taaccttccc ttgctgcta tgaattatct gagagccatg ttcccattta 2200  
tctttttgcc aactatgta ctgttgtaac acctgaaatg gctttgtttt tatcaataaa 2260  
tacttgttga ttgtggtaaa cagc 2284

&lt;210&gt; 86

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (236)... (1024)

&lt;400&gt; 86

tttcgattcc actctcttcc gttctgtgct ctgcagtcgt ccgcgggact ccggccgggt 60  
gccggcccca ggcggtgctt ctccccacca ccgccagct cagctcagcc cagcccagcc 120  
cactctgccc ttagaggccc ttctcccaa agacgcactc cagaagtctc gccctcgtgc 180  
ggctgaggag cctgggatcc cagacctgaa caagtgaac ccccgccct gaaga atg 238

ggc aag acg ttt tcc cag ctg ggc tct tgg cgg gag gat gag aac aag 286

179/307

Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn Lys  
                   5                  10                  15  
 tca atc ctg tcc tcc aaa cca gcc att ggc agc aag gct gtc aac tac 334  
 Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn Tyr  
                   20                  25                  30  
 tcc agc acc ggt agc agc aag tct ttt tgt tcc tgt gtg cct tgt gaa 382  
 Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys Glu  
                   35                  40                  45  
 gga act gct gat gcc agc ttc gtg act tgt ccc acc tgc cag ggc agt 430  
 Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly Ser  
                   50                  55                  60                  65  
 ggc aag att ccc caa gag ctg gag aag cag ttg gtg gct ctc att ccc 478  
 Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile Pro  
                   70                  75                  80  
 tat ggg gac cag agg ctg aag ccc aag cac acg aag ctc ttt gtg ttc 526  
 Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val Phe  
                   85                  90                  95  
 ctg gcc gtg ctc atc tgc ctg gtg acc tcc tcc ttc atc gtc ttt ttc 574  
 Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe Phe  
                   100                  105                  110  
 ctg ttt ccc cgg tcc gtc att gtg cag cct gca ggc ctc aac tcc tcc 622  
 Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser Ser  
  
 Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn Ile

180/307

130	135	140	145	
tta aac atc tcc aat ggc aac tac tac ccc att atg gtg aca cag ctg				718
Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln Leu				
	150	155	160	
acc ctc gag gtt ctg cac ctg tcc ctc gtg gtg ggg cag gtt tcc aac				766
Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser Asn				
	165	170	175	
aac ctt ctc cta cac att ggc cct ttg gcc agt gaa cag atg ttt tac				814
Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe Tyr				
	180	185	190	
gca gta gct acc aag ata cgg gat gaa aac aca tac aaa atc tgt acc				862
Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys Thr				
	195	200	205	
tgg ctg gaa atc aaa gtc cac cat gtg ctt ttg cac atc cag ggc acc				910
Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly Thr				
210	215	220	225	
ctg acc tgt tca tac ctg agc cat tca gag cag ctg gtc ttt cag agc				958
Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln Ser				
	230	235	240	
tat gaa tat gtg gac tgc cga gga aac gca tct gtg ccc cac cag ctg				1006
Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln Leu				
	245	250	255	

181/307

cctgggtctat atctcccaca actccctggg gactaaggaa ggactacaga ggctttgcca 1120  
 aaggagaagc cctgcctcat cacaccctta cctcccaccc cctcagcaca ggaagcttgc 1180  
 tttgaagtta acttcataca cacacactca tatectccag tttccccag attctttcag 1240  
 gggctgccat cagattctgc ccttggttag tttttgttt tttttttgg tagagacaga 1300  
 gtctcactgt tggtcaggt tggttttgaa ctctgggct caagcgatcc tcccttcttg 1360  
 gcctcccaaa gcacttgat tacagatgtg agcctgtgcc tggctggtct ttcttgagga 1420  
 aaatctgacc tggcattttc ttgaggcacc ttagattccc tggagtggca cctggccttt 1480  
 ctgtactgag cacctgggtca gtctgaaggg ggcatttcac cccagctcca tcagggttg 1540  
 cagtccegtc tgaatgtgga gagagctgta gttttatctg gcttttaaaa catggacctg 1600  
 ccggctgggc gcagtggctt acacctgtaa tcccagtact ttgggaggcc gaagtgggtg 1660  
 gatcacttga gggcaggagt tcgtgaccag cctggtcaac atggtgaaac cttgtctcta 1720  
 ctaaaaatac aaaaatt 1737

&lt;210&gt; 87

&lt;211&gt; 1556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (103)... (609)

&lt;400&gt; 87

agcgtcact cgctcgact cagtcgagg aggttcccc gcgcggccg cgccccccc 60

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acg gcc ctg gag gcc ggc agc tgg cgc tgg gga tcc ctg ctc ttc gct	162
Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala	
5 10 15 20	
ctc ttc ctg gct gcg tcc cta ggc aaa gat gca cca tcc aac tgt gtg	210
Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro Ser Asn Cys Val	
25 30 35	
gtg tac cca tcc tcc tcc cag gag agt gaa aac atc acg gct gca gcc	258
Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala	
40 45 50	
ctg gct acg ggt gcc tgc atc gta gga atc ctc tgc ctc ccc ctc atc	306
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu Ile	
55 60 65	
ctg ctc ctg gtc tac aag caa agg cag gca gcc tcc aac cgc cgt gcc	354
Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala	
70 75 80	
cag gag ctg gtg cgg atg gac agc aac att caa ggg att gaa aac ccc	402
Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro	
85 90 95 100	
ggc ttt gaa gcc tca cca cct gcc cag ggg ata ccc gag gcc aaa gtc	450
Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val	
105 110 115	
agg cac ccc ctg tcc tat gtg gcc cag cgg cag cct tct gag tct ggg	498
egg cat ctg ctt teg gag ccc agc acc ccc ctg tct cct cca ggc ccc	546

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Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro

135

140

145

gga gac gtc ttc ttc cca tcc ctg gac cct gtc cct gac tct cca aac 594

Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn

150

155

160

ttt gag gtc atc tagc ccagctgggg gacagtgggc tgttgtggtt gggtctgggg 650

Phe Glu Val Ile

165

caggtgcatt tgagccaggg ctggctctgt gaggggcctc ctgggcctcg gccttggttc 710

cctccctcct gctctgggct cagatactgt gacatcccag aagcccagcc cctcaacccc 770

tctggatgct acatggggat gctggacggc tcagcccctg ttccaaggat tttgggggtc 830

tgagattctc ccctagagac ctgaaattca ccagctacag atgccaaatg acttacatct 890

taagaagtct cagaacgtcc agcccttcag cagctctcgt tctgagacat gaggcttggg 950

atgtggcagc atcagtggga caagatggac actgggccac cctcccaggc accagacaca 1010

gggcacggtg gagagaattc tccccgtgg ccgccttggc tccccgttt tgcccagggc 1070

tgctctctg tcagacttcc tctttgtacc acagtggctc tggggccagg cctgcctgcc 1130

cactggccat cgccaccttc ccagctgcc tctaccagc agtttctctg aagatctgtc 1190

aacagggtta gtcaatctgg ggcttccact gcctgcattc cagtcaccag agcttgggtg 1250

tcccgaacg ggaagtacat attggggcat ggtggcctcc gtgagcaaat ggtgtcttgg 1310

gcaatctgag gccaggacag atgttgcccc acccactgga gatggtgctg agggaggtgg 1370

gtggggcctt ctgggaaggt gaggggagag gggcacctgc cccccgcct cccatcccc 1430

tactcccact gctcagcgcg ggccattgca aggggtgccac acaatgtctt gtccaccctg 1490

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&lt;210&gt; 88

&lt;211&gt; 1855

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (222)... (953)

&lt;400&gt; 88

cagagatgga atttcaccgt gttgcctagg ctggcttgga gctcttgatc tcaagcgatc 60  
 ctccctgcct cggcctccca acgtgctggg attataggcg tgagccaccg ctcttgcca 120  
 gggctctgttc ctagttgcaa cagttcttgg aaaccactc gagaggcca cgcctccatt 180  
 caccaggcca cgcatcaca gaggcaacac caggagccaa c atg agc tcg ggg 233

Met Ser Ser Gly

1

act gaa ctg ctg tgg ccc gga gca gcg ctg ctg gtg ctg ttg ggg gtg 281  
 Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val Leu Leu Gly Val

5

10

15

20

gca gcc agt ctg tgt gtg cgc tgc tca cgc cca ggt gca aag agg tca 329  
 Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly Ala Lys Arg Ser

25

30

35

gag aaa atc tac cag cag aga agt ctg cgt gag gac caa cag agc ttt 377  
 Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp Gln Gln Ser Phe

Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala Trp Pro Gly Pro

185/307

55	60	65	
ctg gcg gac atg gca ccc aca agg aag gac aag ctg ttg caa ttc tac			473
Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu Leu Gln Phe Tyr			
70	75	80	
ccc agc ctg gag gat cca gca tct tcc agg tac cag aac ttc agc aaa			521
Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys			
85	90	95	100
gga agc aga cac ggg tcg gag gaa gcc tac ata gac ccc att gcc atg			569
Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met			
105	110	115	
gag tat tac aac tgg ggg cgg ttc tcg aag ccc cca gaa gat gat gat			617
Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp			
120	125	130	
gcc aat tcc tac gag aat gtg ctc att tgc aag cag aaa acc aca gag			665
Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu			
135	140	145	
aca ggt gcc cag cag gag ggc ata ggt ggc ctc tgc aga ggg gac ctc			713
Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu			
150	155	160	
agc ctg tca ctg gcc ctg aag act ggc ccc act tct ggt ctc tgt ccc			761
Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro			
165	170	175	180

185

190

195



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gca tcc atc cat cag tgg cgc gag tcc agg aag gtc atg ggg caa ctc 857  
 Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu  
 200 205 210  
 cag aga gaa gca tcc cct ggc ccg gtg gga agc cca gac gag gag gac 905  
 Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp  
 215 220 225  
 ggg gaa ccg gat tac gtg aat ggg gag gtg gca gcc aca gaa gcc 950  
 Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala  
 230 235 240  
 tagggcagac caagaagaaa ggagccaagg caaagaggga ccactgtgct catggaccca 1010  
 tcgctgcctt ccaaggacca ttcccagag ctactcaact ttaagcccc tgccatgggt 1070  
 gctcctggaa ggagaaccag ccacctgag gaccacctgg ccatgcgtgc acagcctggg 1130  
 aaaagacagt tactcacggg agctgcaggc ccgtcaccaa gccctctccc gaccaggct 1190  
 ttgtggggca ggcacctggt accaagggtg acccggtccc tggtatggac ggatgcgcag 1250  
 gatttaggat aagctgtcac ccagtcacca taacaaaacc actgtccaac actggtatct 1310  
 gtgttttttt gtgctatgaa ttggattcc taattgctat tgttggttgc tggggtttta 1370  
 aatgattgat aagcttgtac agttaactta tagaggggga gccatattta acattctgga 1430  
 ttccagagta gagatttctg tgttgtctcc tagaaagcat tacatgtagt ttatttcagc 1490  
 atccttggtg ggtggggccc tggtctctct cccctttggt gggacctccc ctttctttgg 1550  
 gcttcagttc actcaggaag aaatgagget gtcgccatct ttatgtgett ccagtggaaa 1610  
 tgtcacttgc tacagacaat agtgcattgag agtctagaga agtagtgacc agaacagggc 1670  
 agagtaggtc cctccatgg cctgaatcc tctctgtct cagggtggc ctctgcagag 1730  
 agttg 1855

187/307

&lt;210&gt; 89

&lt;211&gt; 2530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (28)... (1314)

&lt;400&gt; 89

agcgcggcgg ggcgatgtgt gattacc atg gcg agg agt ctc tgt ccg ggg	51
Met Ala Arg Ser Leu Cys Pro Gly	
1 5	
gcc tgg cta agg aaa ccc tat tac ctc cag gct cgc ttc tca tat gtg	99
Ala Trp Leu Arg Lys Pro Tyr Tyr Leu Gln Ala Arg Phe Ser Tyr Val	
10 15 20	
cgg atg aaa tat ctt ttc ttt tcc tgg tta gtg gtt ttt gtt gga agc	147
Arg Met Lys Tyr Leu Phe Phe Ser Trp Leu Val Val Phe Val Gly Ser	
25 30 35 40	
tgg att ata tat gtg cag tat tct acc tat aca gaa tta tgc aga gga	195
Trp Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly	
45 50 55	
aag gac tgt aag aaa ata ata tgt gac aag tac aag act gga gtt att	243
gat ggg cct gca tgt aac agc ctt tgt gtt aca gaa act ctt tac ttt	291

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Asp Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe  
 75 80 85  
 gga aaa tgt tta tcc acc aag ccc aac aat cag atg tat tta ggg att 339  
 Gly Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile  
 90 95 100  
 tgg gat aat cta cca ggt gtt gtg aaa tgt caa atg gaa caa gcg ctt 387  
 Trp Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu  
 105 110 115 120  
 cat ctt gat ttt gga act gaa ttg gaa cca aga aaa gaa ata gtg cta 435  
 His Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu  
 125 130 135  
 ttt gat aag cca act aga gga act act gta caa aaa ttt aaa gaa atg 483  
 Phe Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met  
 140 145 150  
 gtc tat agt ctc ttt aag gca aaa ttg ggt gac caa gga aac ctc tct 531  
 Val Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser  
 155 160 165  
 gaa ctg gtt aat ctc atc ttg acg gtg gct gat gga gac aaa gat ggc 579  
 Glu Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly  
 170 175 180  
 cag gtt tcc ttg gga gaa gca aag tcg gca tgg gca ctt ctt caa ctg 627  
 Gln Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu  
 Asn Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro

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205	210	215	
aaa tta atg gga ttc tgt ggt gac ctc tat gtg atg gaa agt gtt gaa			723
Lys Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu			
220	225	230	
tat acc tct ctt tat gga ata agc ctt cct tgg gtc att gaa ctt ttt			771
Tyr Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe			
235	240	245	
att cca tct ggg ttc aga aga agc atg gat cag ctg ttc aca cca tca			819
Ile Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser			
250	255	260	
tgg cca aga aag gcc aaa ata gcc ata gga ctt cta gaa ttt gtg gaa			867
Trp Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu			
265	270	275	280
gat gtt ttc cat ggc ccc tac gga aat ttc ctc atg tgc gat act agt			915
Asp Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser			
285	290	295	
gcc aaa aac cta gga tat aat gat aag tat gat ttg aaa atg gtg gat			963
Ala Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp			
300	305	310	
atg aga aaa att gtg cca gag aca aac ctg aaa gaa ctt att aag gat			1011
Met Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp			
315	320	325	
330	335	340	

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act agc tgt gat cag agt aca atg aag tgt act tca gaa gtg ata caa 1107  
 Thr Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln  
 345 350 355 360  
 cca aac ttg gca aaa gct tgt cag tta ctc aaa gac tac cta ctg cgt 1155  
 Pro Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg  
 365 370 375  
 ggt gct cca agt gaa att cgt gaa gaa tta gaa aag cag ctt tat tct 1203  
 Gly Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser  
 380 385 390  
 tgt att gct ctc aaa gtc aca gca aat caa atg gaa atg gaa cat tct 1251  
 Cys Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser  
 395 400 405  
 ttg ata cta aat aac cta aaa aca tta ttg tgg aag aaa att tcc tac 1299  
 Leu Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr  
 410 415 420  
 act aat gac tct tagttcatt tggacataat taccatttta agaaacctgc 1350  
 Thr Asn Asp Ser  
 425  
 cactttttaa gaacaatttt gagcattaaa aaaaaatggc ttcaaattcc tgccagttac 1410  
 acaaaaactcc ttccccccag gcctgagaag ccatcagtat gtgattactg aagtaatggc 1470  
 aggtgtagga tcaacaggtc cccaagatgt cattcctgccc cttttagaag cccgtgttaca 1530  
 tctccgaagt acattcattg tgtaactatt ttgactgact ttaaaaacca atgctgtgaa 1590  
 tactaatgtc ttagcatggt aaagtttgca cattaacaga aattaagact gcaaagcagg 1770

191/307

ttaaacttgc ttctttataa aacagatggt gggtaatag catggtttac tgtattaaag 1830  
acttatacac ccatttttaa cctcattcag acatcaagtt atgtgtagct tcacaatggt 1890  
tcaagtggct tacttcaaga aatcttatac ttgacagtac accaatttta ttgactaaaa 1950  
atggatgaac ttctctaaag attcaaaggc cccatcttag tatcacgcag ctgactgagc 2010  
ccttcaaaac tgacatctta aggcccaatc aagatccaca tatectgatt ttgaactatg 2070  
tgaaagtggg actgttaagt gcaagactaa aataaattat agcagacttt ttagtaataa 2130  
ctttccattt tcaaacagta tatectgtgg gccaaagggc tatttcttaa agaggcatgt 2190  
aaatgtattt atttatctaa tgtttttttc cccatgtaaa ctgatatac aaggtttagt 2250  
atttgcctct ctttcatatt attttcacac gtatactcag atttgcatg tacctttcaa 2310  
catctccata aaattaaaca ccttttggag aaaagatcca ctattttctg ctcaaagggt 2370  
tcgcctacct aaagtgaac atgttaaaaa tctatgtgac catcactgga cagctttctc 2430  
tcaaaacttt ctttcaacgc catggattag caccagtttt gtttacttta aggtactttt 2490  
cccattcctc atctggttat aataaatgga tggaagaaat 2530

&lt;210&gt; 90

&lt;211&gt; 1911

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (232)... (1083)

&lt;400&gt; 90

ttcagagctg tgactgcggc tgcactcaga gaagctgccc ttgctgctc gtagecgccg 180

192/307

gccttctctc ctcgtcatca tccagagcag ccagtgtccg ggaggcagaa g atg ccc 237  
Met Pro  
1

cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc 285  
His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala  
5 10 15

cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg 333  
Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp  
20 25 30

ggg cta gga gag cca cca gag cac act ctc cgg tac ctg gtg ctc cac 381  
Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His  
35 40 45 50

cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg 429  
Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu  
55 60 65

gct gag gag ctg cac cac atc cac tcc agg tac cgg ggc agc tac tgg 477  
Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp  
70 75 80

agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg 525  
Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu  
85 90 95

ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc 573

ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg 621

193/307

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu  
 115 120 125 130  
 aac atc ctc ctg ggc ctc aag ggc ctg gcc cca gct gag atc tct gca 669  
 Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala  
 135 140 145  
 gtg tgt gaa aaa ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca 717  
 Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser  
 150 155 160  
 tat tac atc gga tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg 765  
 Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg  
 165 170 175  
 att cga act tac aat cag cat tac aac aac ctg cta cgg ggt gca gtg 813  
 Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val  
 180 185 190  
 agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg gtg cct gat 861  
 Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp  
 195 200 205 210  
 aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat aaa ctg ccc 909  
 Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro  
 215 220 225  
 cag cag acc gct gac cgt gct ggc atc aag gat cgg gtt tac agc aac 957  
 Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn  
 Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln Met Thr



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245	250	255	
gca gct tct cgc tgt ccc agg agg ttc tcc ggc acc tgc ggc agg agg			1053
Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly Arg Arg			
260	265	270	
aaa agg aag agg tta ctg tgg gca gct tgaagacctc agcgggtgccc			1100
Lys Arg Lys Arg Leu Leu Trp Ala Ala			
275	280		
agtaacctcca cgatgtccca agagcctgag ctctcatca gtggaatgga aaagccccctc			1160
cctctccgca cggatttctc ttgagaccca gggtcaccag gccagagcct ccagtgggtct			1220
ccaagcctct ggactggggg ctctcttcag tggctgaatg tccagcagag ctatttcctt			1280
ccacaggggg cttgcaggg aagggtccag gacttgacat cttagatgc gtcttgtccc			1340
cttgggccag tcatttcccc tctctgagcc tcggtgtctt caacctgtga aatgggatca			1400
taatcactgc cttacctccc tcacggttgt tgtgaggact gagtgtgtgg aagtttttca			1460
taaactttgg atgctagtgt acttaggggg tgtgccaggt gtctttcatg gggccttcca			1520
gacccactec ccacccttct ccccttcctt tgcccgggga cgccgaactc tctcaatggg			1580
atcaacagge tcttgcgcc tctggctcct ggcatgttc cattattggg gagccccage			1640
agaagaatgg agaggaggag gaggetgagt ttgggggtatt gaatcccccg gctcccaccc			1700
tgcagcatca aggttgetat ggactctcct gccgggcaac tcttgctaa tcatgactat			1760
ctctaggatt ctggcaccac ttcttccct gcccccttaa gctagctgt gtatcggcac			1820
ccccaccca ctagagtact cctctcaact tgcggtttcc ttatactcca cccctttctc			1880
aacggtcctt ttttaaagca catctcagat t			1911

&lt;212&gt; PRT

195/307

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145 150 155 160

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

196/307

180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	
Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys			

370

375

380

197/307

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His Ser Leu

385

390

395

400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405

410

415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420

425

430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435

440

445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450

455

460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

&lt;210&gt; 92

&lt;211&gt; 226

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val Gly Gly Phe

1

5

10

15

Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys Val Thr Thr

20

25

30

Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys Arg Pro His

198/307

50	55	60	
Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys Arg Gly Leu			
65	70	75	80
Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe Ala Leu			
	85	90	95
Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala Lys Ala			
100	105	110	
Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser Gly Leu Cys			
115	120	125	
Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr Thr Glu Phe			
130	135	140	
Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly Ala Ala Leu			
145	150	155	160
Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly Gly Val Ile			
	165	170	175
Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg Tyr Thr Tyr			
180	185	190	
Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr His Gly Gly			
195	200	205	
Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp Lys Asn Ala			
210	215	220	
Tyr Val			

199/307

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly

1 5 10 15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg

20 25 30

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu

35 40 45

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe

50 55 60

Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly

65 70 75 80

Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg

85 90 95

Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu

100 105 110

Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly

115 120 125

Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val

130 135 140

Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala



201/307

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu  
1 5 10 15  
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His  
20 25 30  
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val  
35 40 45  
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys  
50 55 60  
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys  
65 70 75 80  
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp  
85 90 95  
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His  
100 105 110  
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile  
115 120 125  
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His  
130 135 140  
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys  
145 150 155 160  
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys  
165 170 175  
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala



202/307

195                      200                      205  
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile  
210                      215                      220  
Ala Ala Cys  
225  
  
<210> 95  
<211> 441  
<212> PRT  
<213> Homo sapiens  
<400> 95  
Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe  
1                      5                      10                      15  
Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser  
20                      25                      30  
Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala  
35                      40                      45  
Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr  
50                      55                      60  
Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp  
65                      70                      75                      80  
Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly

100

105

110

203/307

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala

115

120

125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu

130

135

140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala

145

150

155

160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile

165

170

175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser

180

185

190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp

195

200

205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe

210

215

220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys

225

230

235

240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp

245

250

255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser

260

265

270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala

275

280

285

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

204/307

305                      310                      315                      320  
 Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met  
                          325                      330                      335  
 Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys  
                          340                      345                      350  
 Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser  
                          355                      360                      365  
 Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu  
                          370                      375                      380  
 Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val  
 385                      390                      395                      400  
 Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala  
                          405                      410                      415  
 Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln  
                          420                      425                      430  
 Val Phe Arg Asn Pro Tyr Val Trp Asp  
                          435                      440

&lt;210&gt; 96

&lt;211&gt; 265

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

205/307

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro

20

25

30

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val

35

40

45

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser

50

55

60

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser

65

70

75

80

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys

85

90

95

Ser Gly Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser

100

105

110

Gln Glu Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp

115

120

125

Leu Leu Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp

130

135

140

Asn Gly Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg

145

150

155

160

Asp Asp Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met

165

170

175

Glu Ile Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile

180

185

190

Cys Ile Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe

206/307

210 215 220  
Leu Leu Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr  
225 230 235 240  
Val Glu Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser  
245 250 255  
Leu Lys Ile Thr Asn Asp Tyr Ile Phe  
260 265

&lt;210&gt; 97

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe  
1 5 10 15  
Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu  
20 25 30  
Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln  
35 40 45  
Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His  
50 55 60  
Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala

85

90

95

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His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg

100

105

110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp

115

120

125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe

130

135

140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro

145

150

155

160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu

165

170

175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser

180

185

190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln

195

200

205

&lt;210&gt; 98

&lt;211&gt; 400

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met Ala Trp Arg Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu

1

5

10

15

Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp

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35 40 45  
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe  
50 55 60  
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro  
65 70 75 80  
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe  
85 90 95  
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu  
100 105 110  
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala  
115 120 125  
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly  
130 135 140  
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val  
145 150 155 160  
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln  
165 170 175  
Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val  
180 185 190  
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe  
195 200 205  
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile

225

230

235

240

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Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys

245

250

255

His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys

260

265

270

Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys

275

280

285

His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg

290

295

300

Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp

305

310

315

320

Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro

325

330

335

Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp

340

345

350

Gly Ser Asp Glu Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu

355

360

365

Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala

370

375

380

Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser

385

390

395

400

&lt;210&gt; 99

&lt;213&gt; Homo sapiens



210/307

&lt;400&gt; 99

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr

1 5 10 15

Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val

20 25 30

His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu

35 40 45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His

50 55 60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro

65 70 75 80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys

85 90 95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly

100 105 110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys

115 120 125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met

130 135 140

Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser Thr

145 150 155 160

Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg

180

185

190

211/307

&lt;210&gt; 100

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 100

Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly

1 5 10 15

Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu

20 25 30

Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro

35 40 45

Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro

50 55 60

Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala

65 70 75 80

His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln

85 90 95

Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val

100 105 110

Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp

115 120 125

Asp Ala Ala Asp Ala Ala Glu Leu Ala Arg Ala Leu Leu Arg Ala Arg

Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro

212/307

145                      150                      155                      160  
 Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala  
                          165                      170                      175  
 Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro  
                          180                      185                      190  
 Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp  
                          195                      200                      205  
 Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His  
                          210                      215                      220  
 Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu  
 225                      230                      235                      240  
 Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg  
                          245                      250                      255  
 Leu Leu Pro Pro  
                          260

&lt;210&gt; 101

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

atggttgggtg ccatgtggaa ggtgattggtt tgcctgggtcc tgttgatgcc tggeccctgt 60

agtttgggtcg gccctttccc aggactgaac atgaagagtt atgcccgttt cctcaccgtg 240

213/307

aataagaactt acaacagcaa cctcttcttc tggttcttcc cagctcagat acagccagaa	300
gatgccccag tagttctctg gctacagggt gggccgggag gttcatccat gtttggaactc	360
tttgtggaac atgggcctta tgttgtcaca agtaacatga ccttgcgta cagagacttc	420
ccctggacca caacgtctc catgctttac attgacaatc cagtgggcac aggcttcagt	480
tttactgatg ataccacagg atatgcagtc aatgaggacg atgtagcacg ggatttatac	540
agtgcactaa ttcagttttt ccagatatct cctgaatata aaaataatga cttttatgtc	600
actggggagt cttatgcagg gaaatatgtg ccagccattg cacacctcat ccattccctc	660
aacctgtga gagaggtgaa gatcaacctg aacggaattg ctattggaga tggatatctt	720
gatcccgaa caattatagg gggtatgca gaattcctgt accaaattgg cttgttgat	780
gagaagcaaa aaaagtactt ccagaagcag tgccatgaat gcatagaaca catcaggaag	840
cagaactggt ttgaggectt tgaaatactg gataaactac tagatggcga cttacaagt	900
gatecttctt acttccagaa tgttacagga tgtagtaatt actataactt tttgcggtgc	960
acggaacctg aggatcagct ttactatgtg aaatttttgt cactcccaga ggtgagacaa	1020
gccatccacg tggggaatca gacttttaat gatggaacta tagttgaaaa gtacttgca	1080
gaagatacag tacagtcagt taagccatgg ttaactgaaa tcatgaataa ttataaggtt	1140
ctgatctaca atggccaact ggacatcacc gtggcagctg cctgacaga gcactccttg	1200
atgggcatgg actggaaagg atcccaggaa tacaagaagg cagaaaaaaaa agtttggaag	1260
atcttttaat ctgacagtga agtggtgtgt tacatccggc aagcgggtga ctccatcag	1320
gtaattatc gaggtggagg acatatctta cctatgacc agcctctgag agcttttgac	1380
atgattaatc gattcattta tggaaaagga tgggactcct atgttgga	1428

(210) 102

(213) Homo sapiens

214/307

&lt;400&gt; 102

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 acttgggttt accagggtct gtggatgaac tgcgcaggta acgcgttggg ttctttccat 180  
 tgccgaccgc attttactat ctcaaagta gcaggttata tacaggcatg tagaggactt 240  
 atgatcgtg ctgtcagcct gggtctcttt ggttccatat ttgcgctctt tggaatgaag 300  
 tgtaccaaag tcggaggctc cgataaagcc aaagctaaaa ttgcttggtt ggctgggatt 360  
 gtattcatac tgtcagggt gtgtcaatg actggatgtt cctatatgc aaacaaaac 420  
 acaacggaat tctttgatec tctctttgtt gagcaaaagt atgaattagg agccgctctg 480  
 tttattggat gggcaggagc ctactgtgc ataattggtg gtgtcatatt ttgcttttca 540  
 atatctgaca acaacaaaac acccagatac acatacaacg ggccacacac tgatcatgtc 600  
 tctcgacaaa agtatcatgg tggagaagat tttaaaacaa caaaccttc aaaacagttt 660  
 gataaaaatg cttatgtc 678

&lt;210&gt; 103

&lt;211&gt; 915

&lt;212&gt; DNA

· 213 · Homo sapiens

&lt;400&gt; 103

atggggatcc agacgagccc cgtcttctg gccctccctgg ggggtggggt ggtaactctg 60  
 ctcggcctgg ctgtgggtc ctacttgggt cggaggctcc gccggcctca ggtaactctc 120  
 ctggacccca atgaaaagta cctgctacga ctgctagaca agacgactgt gaccacaaac 180  
 gtcaccagt atgaggatca aggetatgt gatcttgta tcaaggteta cctgaagggt 360

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gtgcacccca aatttctga gggaggggaag atgtctcagt acctggatag cctgaaggtt 420  
 ggggatgttg tggagtttcg ggggcccaagc gggttgctca cttacactgg aaaagggeat 480  
 tttacatttc agcccaacaa gaaatctcca ccagaacccc gagtggcgaa gaaactggga 540  
 atgattgccg gcgggacagg aatcacccca atgtctacagc tgatccgggc catcctgaaa 600  
 gtccctgaag atccaaccca gtgctttctg ctttttgcca accagacaga aaaggatata 660  
 atcttgccgg aggacttaga ggaactgcag gccgcctata ccaatcgctt taagctctgg 720  
 ttcactctgg atcatccccc aaaagattgg gcctacagca agggctttgt gactgccgac 780  
 atgatccggg aacacctgcc cgtccaggg gatgatgtgc tgggtactgct ttgtgggcca 840  
 ccccaatgg tgcagctggc ctgccatccc aactgggaca aactgggcta ctacaaaaag 900  
 atgcgattca cctac 915

&lt;210&gt; 104

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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 ctcttttggc agggccttga agttttctac ccagagttag ggaacattgg ctgcaaggtt 180  
 gtctctgatt gtaacaacta cagacagaag atcacctctt ggatggagcc gatagtcaag 240  
 ttcccggggg ccgtggacgg cgcaacctat atcttggtga tgggtgatcc agatgccctt 300  
 agcagagcag aaccagaca gagattctgg agacattggc tggtaacaga tatcaagggc 360

gtcctctctc tcttctccaa ggaaaacaaa actcgagget cttggaaaat ggacagattt 540

216/307

ctgaaccgtt tccacctggg cgaacctgaa gcaagcacc agttcatgac ccagaactac 600  
 caggactcac caacctccca ggctcccaga gaaagggcc a gcagcccaa gcacaaaaac 660  
 caggcgagaga tagctgcctg c 681

&lt;210&gt; 105

&lt;211&gt; 1323

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

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 aacctgtgtg accgctctgg ggcgtagggc atcgctctgg aggcctgggc tggggcgggc 180  
 attgtaacca cgtttgtgt caccatcacc ctggtaggca gectccctt tgtgcaggac 240  
 accaagaaac ggagcctgt ggggaccag gtattcttcc ttctggggac cctgggctc 300  
 ttctgccteg tgtttgcctg tgtggtgaag cccgacttct ccacctgtgc ctctcggcgc 360  
 ttcctctttg gggttctgtt cgccatctgc ttctcttgtc tggcggtca cgtctttgcc 420  
 ctcaacttcc tggcccggaa gaaccacggg ccccggggt gggtagctt cactgtggct 480  
 ctgtctgtga cctggtaga ggtcatcacc aatacagagt ggtgatcat cacctggtt 540  
 cggggcagtg gcgagggcgg cctcagggc aacagcagc caggctgggc cgtggcctcc 600  
 cctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgtgtgtg 660  
 ctgggtgcct tctgggggc ctggccgcc ctgtgtggcc gctacaagc ctggcgtaag 720  
 catggggtct ttgtgtctt caccacagcc acctccgtt ccatatgggt ggtgtggatc 780

ctccagtgga ccaagtcag cccagagcaa agctaccagg gggacatgta cccacccgg 960

217/307

ggcggtgggct atgagaccat cctgaaagag cagaagggtc agagcatgtt cgtggagaac 1020  
 aaggcctttt ccatggatga gccggttgca gctaagaggc cgggtgtcacc atacagcggg 1080  
 tacaatgggc agctgtgtgac cagtgtgtac cageccactg agatggccct gatgcacaaa 1140  
 gtccggtccg aaggagctta cgacatcacc ctcccacggg ccaccgcca cagccaggtg 1200  
 atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcggccca gagccaccag 1260  
 gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaacce ctacgtgtgg 1320  
 gac 1323

&lt;210&gt; 106

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

atggccgctg ccgtcccga gaggatgagg gggccagcac aagcgaaact gctgcccggg 60  
 teggceatcc aagcccttgt ggggttggeg cggcgctgg tcttggegt cctgcttgtg 120  
 tccgcgctc tatccagtgt tgtatcagg actgattcac cgagcccaac cgtactcaac 180  
 tcacatattt ctaccccaaa tgtgaatgt ttaacacatg aaaaccaaac caaaccttct 240  
 atttcccaaa tcagcaccac cctccctccc acgacagta ccaagaaaag tggaggagca 300  
 tetgttggtc ctcatccctc gctactcct ctgtctcaag aggaagctga taacaatgaa 360  
 gatcctagta tagaggagga ggatcttctc atgtgaaca gttctccatc cacagccaaa 420  
 gacactctag acaatggcga ttatggagaa ccagactatg actggaccac gggccccagg 480  
 gacgacgacg agtctgatga caccttggaa gaaaacaggg gttacatgga aattgaacag 540

aggaagattt ttctcttggg tcaaagcagg aatggcgtg atggccttgg tccaaaaca

aggaagattt ttctcttggg tcaaagcagg aatggcgtg atggccttgg tccaaaaca 720



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gtggaatacc atcgccctaga tcagaatgtt aatgaggcaa tgccttcttt gaagattacc 780

aatgattata ttttt 795

<210> 107

<211> 624

<212> DNA

<213> Homo sapiens

<400> 107

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gtccgtgacc tctagctga gcagcgcttc ccgggcgcgc tgcctgcctc ggacttggac 180

ctgctgttgc acatgaacaa cgcgcgctac ctgcgcgagg ccgactttgc gcgcgtcgcg 240

cacctgaccc gctgcggggg gctcggggcg ctgagggagt tgcgggcgca cacggtgctg 300

ggggcctcgt gcgcgcgcca ccgcgcctcg ctgcgcctgc tggagccctt cgaggtgcgc 360

acccgcctgc tgggctggga cgaccgcgcg ttctacctgg aggcgcgctt tgtcagcctg 420

cgggacgggt tcgtgtgcgc gctgctgcgc ttccggcagc acctgctggg cacctcacc 480

gagcgcgtcg tgcagcacct gtgccagcgc aggggtggagc cccctgagct gcccgctgat 540

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ctcagtgatg tcaccaagga ccag 624

<210> 108

<211> 1200

<400> 108

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atggcgtggc ggcggcgcca agccagcgtc ggggctcgcg gcgtgttggc tctggcgttg	60
ctcgccctgg cctgtgcgt gcccggggcc cggggccggg ctctcgagt gttctcgccc	120
gtggtaaaca tcgagtacgt ggaccgcag accaacctga cgggtgtggag cgtctcgga	180
agtggccgt tcggcgacag ctgcccgaag gagggcgcg atggcctggt gggcgcccc	240
tgggcgcccc ggggagacct cgagggtgc ggcgccgaca cgcgtttctt cgtgccccg	300
cccgcgggcc gagggcgcc gccctgggtc gccctggtgg ctggtggggg ctgcacctc	360
aaggacaagg tctgtgtggc ggcgcggagg aacgcctcgg ccgtcgctct ctacaatgag	420
gagcgtacg ggaacatcac ctgcccattg tctcgcggg gaacaggaaa tatagtggtc	480
attatgatta gctatccaaa aggaagagaa attttgagc tggtgcaaaa aggaattcca	540
gtaacgatga ccataggggt tggcaccgg catgtacagg agtcatcag cggtcagtct	600
gtggtgtttg tggccattgc ctcatcacc atgatgatta tctcgttagc ctggctaata	660
ttttactata tacagcgttt cctatatact ggctctcaga ttggaagtc gagccataga	720
aaagaaacta agaaagttat tggccagctt ctacttcata ctglaaagca tggagaaaag	780
ggaattgatg ttgatgtga aaattgtgca gtgtgtattg aaaatttcaa agtaaaggat	840
attattagaa ttctgccatg caagcatatt ttcatagaa tatgcattga cccatggctt	900
ttggatcacc gaacatgtcc aatgtgtaaa ctgatgtca tcaaagccct aggatattgg	960
ggagagcctg gggatgtaca ggagatgect gctccagaat ctctctctgg aagggatcca	1020
gttgcaaatt tgagtctagc ttaccagat gatgacggaa gtgatgagag cagtcacca	1080
tcagctccc ctgctgaate tgagccacag tggatccca gctttaaagg agatgcagga	1140
gaaaatacgg cattgctaga agccggcagg agtgactctc ggcattggagg acccatctcc	1200

&lt;210&gt; 109

&lt;213&gt; Homo sapiens

220/307

&lt;400&gt; 109

atgttttgcc cactgaaact catcctgctg ccagtgttac tggattatc cttgggcctg	60
aatgacttga atgtttcccc gcctgagcta acagtcctatg tgggtgattc agctctgatg	120
ggatgtgttt tccagagcac agaagacaaa tgtatattca agatagactg gactctgtca	180
ccaggagagc acgccaagga cgaatatgtg ctatactatt actccaatct cagtgtgcct	240
attgggcgct tccagaaccg cgtacacttg atgggggaca acttatgcaa tgatggctct	300
ctcctgctcc aagatgtgca agaggctgac cagggaacct atatctgtga aatccgcctc	360
aaaggggaga gccaggltgt caagaaggcg gtggtactgc atgtgcttcc agaggagccc	420
aaagagctca tggtecatgt ggggtggattg attcagatgg gatgtgtttt ccagagcaca	480
gaagtgaac acgtgaccaa ggtagaatgg atattttcag gacggcgccg aaaghtaaca	540
aggaggaaac atcactgtgt tagagaaggc tctggc	576

&lt;210&gt; 110

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

atggcgggggt cgcgcctgct ctgggggccc cgggcgcggg gcgtcgccct ttgtgtgctg	60
ctgtgtctcg gctgtttcg gcgcgcgcgc gcgtctctcg cgcggccggt aaaggagccc	120
cgcggcctaa gcgcagcgtc tccgcccttg gctgagactg gcgtccctcg ccgcttcggg	180
cggtcagtgc cccgaggtga ggccggcggg gcgggtgcagg agctggcgcg ggcgctggcg	240
catctgtgga aggcgcgaac tcaggagcgg gcgcgggccc aggcgcagga ggctgaggat	300
ctccgcgcgc gccttgaccc tgcgcgcctc gcgcgcgcgc ttgtccccc gcgcgtcccc	480

221/307

gcccgcggcgc tccgaccccg gcccccggtc tacgacgacg gccccgcggg cccggatgct 540  
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 cggattcttg cgggaagcgc ggactccgag ggggtggcag ccccgcgccg cctccgccgt 660  
 gccgcccagc acgatgtggg ctctgagctg cccctgagg gcgtgctggg ggcgctgctg 720  
 cgtgtgaaac gcctagagac cccggcgccc caggtgcctg cagccgcct cttgccaccc 780

&lt;210&gt; 111

&lt;211&gt; 1633

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (68)... (1498)

&lt;400&gt; 111

acaaccggct ggggtccttg cgcgcgcgg ctcagggagg agcaccgact gcgcgcacc 60  
 ctgagag atg gtt ggt gcc atg tgg aag gtg att gtt tgc ctg gtc ctg 109

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu

1

5

10

ttg atg cct gcc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt 157  
 Leu Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser

15

20

25

30

gtt tcc atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc 205

cct tac att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg 253

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Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu  
 50 55 60  
 gtc ggc cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc 301  
 Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu  
 65 70 75  
 acc gtg aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca 349  
 Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro  
 80 85 90  
 gct cag ata cag cca gaa gat gcc cca gta gtt ctc tgg cta cag ggt 397  
 Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly  
 95 100 105 110  
 ggg ccg gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct 445  
 Gly Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro  
 115 120 125  
 tat gtt gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg 493  
 Tyr Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp  
 130 135 140  
 acc aca acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc 541  
 Thr Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly  
 145 150 155  
 ttc agt ttt act gat gat acc cac gga tat gca gtc aat gag gac gat 589  
 Phe Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp  
 Val Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe



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cgg tgc acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca	1069
Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser	
320 325 330	
ctc cca gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat	1117
Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn	
335 340 345 350	
gat gga act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca	1165
Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser	
355 360 365	
gtt aag cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc	1213
Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile	
370 375 380	
tac aat ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cac	1261
Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His	
385 390 395	
tcc ttg atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca	1309
Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala	
400 405 410	
gaa aaa aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt	1357
Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly	
415 420 425 430	
tac atc cgg caa gcg ggt gac ttc cat cag gta att att cga ggt gga	1405
gga cat att tta ccc tat gac cag cct ctg aga gct ttt gac atg att	1453

225/307

Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile

450

455

460

aat cga ttc att tat gga aaa gga tgg gat cct tat gtt gga taaac 1500

Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

taccttccca aaagagaaca tcagaggttt tcattgctga aaagaaaatc gtaaaaacag 1560

aaaatgtcat aggaataaaa aaattatctt ttcatatctg caagatTTTT ttcatcaata 1620

aaaattatcc ttg 1633

&lt;210&gt; 112

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (192)... (872)

&lt;400&gt; 112

ctttaaaatg tcattggtaa accatacttg atcctaaatt cctgtacttc ctgaggecat 60

ccgagcatga aacgtgtgca cctaccacaa tccgttggt gtgacgttg tcaaagtgtt 120

ctctateggc tgcattgcta gaccacaaa gcgttctgac cggacagtgt cactggagaa 180

ggcggcgcga c atg tcc agg gcg cag atc tgg gct ctg gtg tct ggt gtc 230

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val

Gly Gly Phe Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys



226/307

15	20	25	
gtg acc acg cga gcc tcc tcg gtg ata aca gcc act tgg gtt tac cag			326
Val Thr Thr Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln			
30	35	40	45
ggg ctg tgg atg aac tgc gca ggt aac gcg ttg ggt tct ttc cat tgc			374
Gly Leu Trp Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys			
50	55	60	
cga ccg cat ttt act atc ttc aaa gta gca ggt tat ata cag gca tgt			422
Arg Pro His Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys			
65	70	75	
aga gga ctt atg atc gct gct gtc agc ctg ggc ttc ttt ggt tcc ata			470
Arg Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile			
80	85	90	
ttt gcg ctc ttt gga atg aag tgt acc aaa gtc gga ggc tcc gat aaa			518
Phe Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys			
95	100	105	
gcc aaa gct aaa att gct tgt ttg gct ggg att gta ttc ata ctg tca			566
Ala Lys Ala Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser			
110	115	120	125
ggg ctg tgc tca atg act gga tgt tcc cta tat gca aac aaa atc aca			614
Gly Leu Cys Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr			
130	135	140	
145	150	155	

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gcc gct ctg ttt att gga tgg gca gga gcc tca ctg tgc ata att ggt 710  
 Ala Ala Leu Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly  
 160 165 170  
 ggt gtc ata ttt tgc ttt tca ata tct gac aac aac aaa aca ccc aga 758  
 Gly Val Ile Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg  
 175 180 185  
 tac aca tac aac ggg gcc aca tct gtc atg tct tct cgg aca aag tat 806  
 Tyr Thr Tyr Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr  
 190 195 200 205  
 cat ggt gga gaa gat ttt aaa aca aca aac cct tca aaa cag ttt gat 854  
 His Gly Gly Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp  
 210 215 220  
 aaa aat gct tat gtc t aaaagagctc gcgggcaagc tgccctcttga 900  
 Lys Asn Ala Tyr Val  
 225  
 gtttggttata aaagcgaact gttcacaaaa tgateccatc aaggeccctcc cataattaac 960  
 actcaaaaact atttttaaaa tatgcatttg aagcatctgt tgattgtatg gatgtaagtg 1020  
 ttcttacata gttagtata tactaatcat ttctgttgt ggctttctat aaaaaataaa 1080  
 cagtttatit acagg 1095

&lt;210&gt; 113

&lt;211&gt; 1602

&lt;220&gt;

228/307

&lt;221&gt; CDS

&lt;222&gt; (34)... (951)

&lt;400&gt; 113

tttgtcaggt ggtggaggaa aaggcgctcc gtc atg ggg atc cag acg agc ccc 54

Met Gly Ile Gln Thr Ser Pro

1

5

gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg 102

Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu

10

15

20

gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act 150

Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr

25

30

35

ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg cta gac aag acg 198

Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr

40

45

50

55

act gtg agc cac aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc 246

Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala

60

65

70

cac cac act ctg ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc 294

His His Thr Leu Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr

75

80

85

cga att gat ggc agc ctg gtc atc agg cca tac act cct gtc acc agt 342

gat gag gat caa ggc tat gtg gat ctt gtc atc aag gtc tac ctg aag 390

229/307

Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys Val Tyr Leu Lys  
 105 110 115  
 ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg tct cag tac ctg 438  
 Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met Ser Gln Tyr Leu  
 120 125 130 135  
 gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg ggg cca agc ggg 486  
 Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg Gly Pro Ser Gly  
 140 145 150  
 ttg ctc act tac act gga aaa ggg cat ttt aac att cag ccc aac aag 534  
 Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile Gln Pro Asn Lys  
 155 160 165  
 aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg gga atg att gcc 582  
 Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu Gly Met Ile Ala  
 170 175 180  
 ggc ggg aca gga atc acc cca atg cta cag ctg atc cgg gcc atc ctg 630  
 Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile Arg Ala Ile Leu  
 185 190 195  
 aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt ttt gcc aac cag 678  
 Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu Phe Ala Asn Gln  
 200 205 210 215  
 aca gaa aag gat atc atc ttg cgg gag gac tta gag gaa ctg cag gcc 726  
 Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu Glu Leu Gln Ala  
 Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu Asp His Pro Pro

230/307

235	240	245	
aaa gat tgg gcc tac agc aag ggc ttt gtg act gcc gac atg atc cgg			822
Lys Asp Trp Ala Tyr Ser Lys Gly Phe Val Thr Ala Asp Met Ile Arg			
250	255	260	
gaa cac ctg ccc gct cca ggg gat gat gtg ctg gta ctg ctt tgt ggg			870
Glu His Leu Pro Ala Pro Gly Asp Asp Val Leu Val Leu Leu Cys Gly			
265	270	275	
cca ccc cca atg gtg cag ctg gcc tgc cat ccc aac ttg gac aaa ctg			918
Pro Pro Pro Met Val Gln Leu Ala Cys His Pro Asn Leu Asp Lys Leu			
280	285	290	295
ggc tac tca caa aag atg cga ttc acc tac tg agcatcctcc agcttcctg			970
Gly Tyr Ser Gln Lys Met Arg Phe Thr Tyr			
300	305		
gtgctgttcg ctgcagttgt tccccatcag tactcaagca ctataagcct tagattcctt			1030
tcttcagagt ttcaggtttt ttcagttaca tctagagctg aaatctggat agtacctgca			1090
ggaacaatat tctgtagcc atggaagagg gccaaaggctc agtcactcct tggatggcct			1150
cctaaatctc cccgtggcaa caggctccagg agaggcccat ggagcagttc cttccatgga			1210
glaagaagga agggagcatg tacgcttggt ccaagattgg ctagttcctt gatagcatct			1270
tactctcacc ttctttgtgt ctgtgatgaa aggaacagtc tgtgcaatgg gttttactta			1330
aacttcactg ttcaacctat gagcaaatct glatgtgtga gtataagttg agcatagcat			1390
acttccagag gtggtcttat ggagatggca agaaaggagg aaatgatttc ttcagatctc			1450
aaaggagtct gaaatatcat atttctgtgt gtgtctctct cagccctgc ccaggctaga			1510

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&lt;210&gt; 114

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (99)... (782)

&lt;400&gt; 114

agtcctccca aagtacttgt glccgggtgg tggactggat tcgctgcgga gccctggaag 60

ctgcctttcc ttctccctgt gcttaaccag aggtgccc atg ggt tgg aca atg 113

Met Gly Trp Thr Met

1

5

agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg gtg gtc act 161

Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr

10

15

20

gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc ttg gac 209

Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp

25

30

35

gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca gag ttg 257

Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu

40

45

50

ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac aga cag 305

aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg gcc gtg 353

232/307

Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val  
 70 75 80 85  
 gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc cct agc 401  
 Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser  
 90 95 100  
 aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta aca gat 449  
 Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp  
 105 110 115  
 atc aag ggc gcc gac ctg aag aaa ggg aag att cag ggc cag gag tta 497  
 Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu  
 120 125 130  
 tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc cat cgc 545  
 Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg  
 135 140 145  
 tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct ctc ctt 593  
 Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu  
 150 155 160 165  
 ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga ttt ctg 641  
 Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe Leu  
 170 175 180  
 aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc atg acc 689  
 Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe Met Thr  
  
 Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Glu Arg Ala

233/307

200	205	210	
agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc tgc t			780
Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala Cys			
215	220	225	
agatagccgg ctttgcctc cgggcatgtg gccacactgc ccaccaccga cgatgtgggt			840
atggaacccc ctctggatac agaaccctt cttttccaaa taaaaaaaa atcatcc			897

&lt;210&gt; 115

&lt;211&gt; 1866

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (142)... (1467)

&lt;400&gt; 115

gcccgcctgc gggggcgtgg cagtcaacag caacaacca cagcccgga gggccagaaa	60
ctcccatctc cctcaccagc cggaaagtac gagtcggctc agcctggagg gacccaacca	120
gagcctggcc tgggagccag g atg gcc atc cac aaa gcc ttg gtg atg tgc	171

Met Ala Ile His Lys Ala Leu Val Met Cys

1	5	10	
ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag gcc cat			219
Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly His			

Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu



234/307

30	35	40	
tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct ggg			315
Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala Gly			
45	50	55	
gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc agc			363
Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala Ser			
60	65	70	
ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc cag			411
Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln			
75	80	85	90
gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt gcc			459
Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe Ala			
95	100	105	
tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct egg cgc ttc ctc			507
Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu			
110	115	120	
ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac gtc			555
Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His Val			
125	130	135	
ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc tgg			603
Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly Trp			
140	145	150	
155	160	165	170

235/307

aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag ggc	699
Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu Gly	
175 180 185	
ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc tgt	747
Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro Cys	
190 195 200	
gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg ctg	795
Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met Leu	
205 210 215	
ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc cgc	843
Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg	
220 225 230	
tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca gcc	891
Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr Ala	
235 240 245 250	
acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac ggc	939
Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr Gly	
255 260 265	
aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc atc	987
Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile	
270 275 280	
gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc	1035
gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag ggc	1083

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Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly  
 300 305 310  
 gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa gag 1131  
 Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu  
 315 320 325 330  
 cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg gat 1179  
 Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met Asp  
 335 340 345  
 gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac aat 1227  
 Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn  
 350 355 360  
 ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg atg 1275  
 Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu Met  
 365 370 375  
 cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg gcc 1323  
 His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala  
 380 385 390  
 acc gcc aac agc cag gtg atg ggc agt gcc aac tgg acc ctg cgg gct 1371  
 Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg Ala  
 395 400 405 410  
 gaa gac atg tac tgg gcc cag agc cac cag gcg gcc aca ccg ccg aaa 1419  
 Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro Lys  
  
 Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp

237/307

430	435	440	
tgagtc agcgggtggcg aggagaggcg gtcggatttg gggagggccc tgaggacctg			1520
gccccgggca agggactctc caggctcctc ctccccctgg caggcccagc aacatgtgcc			1580
ccagatgttg aagggcctcc ctctctgcca gtgtttgggt ggggtgcatg ggtgtcccca			1640
cccactcctc agtgtttgtg gagtcgagga gccaacccca gcctcctgcc aggatcacct			1700
cggcgggtcac actccagcca aatagtgttc tcgggggtgtt ggctgggcag cgcctatgtt			1760
ttctctggaga ttcttgcaac ctcaagagac ttcccaggcg ctcaggcctg gatcttgcct			1820
ctctgtgagg aacaagggtg cctaataaat acatttctgc tttatt			1866

&lt;210&gt; 116

&lt;211&gt; 2198

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)... (847)

&lt;400&gt; 116

aaaatggcgt agagcctagc aacagegcag gctcccagcc gagtcggtt atg gcc	55
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Met Ala

1

gct gcc gtc ccg aag agg atg agg ggg cca gca caa gcg aaa ctg ctg	103
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Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu

Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val

238 / 307

20	25	30	
ttg gcg ctc ctg ctt gtg tcc gcc gct cta tcc agt gtt gta tca cgg			199
Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg			
35	40	45	50
act gat tca ccg agc cca acc gta ctc aac tca cat att tct acc cca			247
Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser Thr Pro			
55	60	65	
aat gtg aat gct tta aca cat gaa aac caa acc aaa cct tct att tcc			295
Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser Ile Ser			
70	75	80	
caa atc agc acc acc ctc cct ccc acg acg agt acc aag aaa agt gga			343
Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly			
85	90	95	
gga gca tct gtg gtc cct cat ccc teg cct act cct ctg tct caa gag			391
Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser Gln Glu			
100	105	110	
gaa gct gat aac aat gaa gat cct agt ata gag gag gag gat ctt ctc			439
Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu			
115	120	125	130
atg ctg aac agt tct cca tcc aca gcc aaa gac act cta gac aat ggc			487
Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly			
135	140	145	
150	155	160	

239/307

gac gag tct gat gac acc ttg gaa gaa aac agg ggt tac atg gaa att 583

Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile

165

170

175

gaa cag tca gtg aaa tct ttt aag atg cca tcc tca aat ata gaa gag 631

Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile Glu Glu

180

185

190

gaa gac agc cat ttc ttt ttt cat ctt att att ttt gct ttt tgc att 679

Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe Cys Ile

195

200

205

210

gct gtt gtt tac att aca tat cac aac aaa agg aag att ttt ctt ctg 727

Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe Leu Leu

215

220

225

gtt caa agc agg aaa tgg cgt gat ggc ctt tgt tcc aaa aca gtg gaa 775

Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr Val Glu

230

235

240

tac cat cgc cta gat cag aat gtt aat gag gca atg cct tct ttg aag 823

Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser Leu Lys

245

250

255

att acc aat gat tat att ttt taaagc actgtgattt gaatttgctt 870

Ile Thr Asn Asp Tyr Ile Phe

260

265

atgtaatttt atttgcttga ctttttatat gatattgtgc aaatgtttgc cataggcaat 930

atgtgagtta aacattacct tatatttaca ctgttagttt ttattgtttt agatttatta 1110

240/307

tgcttcttct ggaagtatta gtgatgctac ttttaaaaga teccaaactt gtaactaaat	1170
tctgacatat ctgttactgc tgactcacat tcattctccg ccattcaaact actatTTTTT	1230
atccacattt ttttttggtc ccaaactgta atgtacaagg atatgtgtga taatgctttg	1290
gatttgagta atatTTTTT ttcttccaag aaaactgctt tggatatttt tagataattt	1350
aaacataatt taggataatg atattgctca atctgaccac aatttttaggt aaaacattaa	1410
atgtgtcaag aaatcttggc aacagagact ctgcagcttg cagtggacat agataaaatg	1470
ttacagagat actatTTTTT tggttggaat tactatatta aatttagaag cagaaactgg	1530
taaaatgtta aatacatgta caattgcttt tagttagcaa ttgattgtag catgggttcc	1590
tccaagggtt caagcaatgg gcagagttta aaattatata agattcggtt acttcgttta	1650
ttattttaca gtaaatttga ataaatctta ggggtcatta tcaattaaat aatactgtac	1710
ctaggtcttt caaattaaaa ttatacctga atgaagttgt ttgtatacat aaaggatatt	1770
tgtgtacaat taactTTTTT cccccacaet tgttttcttt gtttttggtt ttataggcaa	1830
ctggaaagta ttactatgg gattcattta tgtctgtctt tctatcataa agaattgatc	1890
aatatgtaaa tatgtgattt gaaccatggt tgacttacaa gtgtcactac agcttttttag	1950
aaaacatagc cctaatatat gttaaagcagg acccggttga gccagtgggc ttgcgcttta	2010
tgtagagctg gaagaaggcc gtccatcctg tctcttgggc ggacagtgtg ctctccta	2070
agggaaggga agcacaatgg aaataccctt gaaccgtttt attgcagtaa ttttttcat	2130
atctgaaact attattttaat attttgaata agatttttaa aaataaatgg caaagatata	2190
aatctatg	2198

&lt;210&gt; 117

&lt;211&gt; 2180

&lt;220&gt;

241/307

&lt;221&gt; CDS

&lt;222&gt; (69)... (695)

&lt;400&gt; 117

aaccagcgcc gcggacaccg gcaccggcgc cacggactcc gcaggacccc gcgcccgcgc 60

ccgceget atg ctg ggg ctg ctg gtg gcg ttg ctg gcc ctg ggg ctc gct 110

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala

1

5

10

gtc ttt gcg ctg ctg gac gtc tgg tac ctg gtg cgc ctt ccg tgc gcc 158

Val Phe Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala

15

20

25

30

gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta gct 206

Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala

35

40

45

gag cag cgc ttc ccg ggc cgc gtg ctg ccc tgc gac ttg gac ctg ctg 254

Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu

50

55

60

ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg cgc 302

Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg

65

70

75

gtc gcg cac ctg acc cgc tgc ggg gtg ctc ggg gcg ctg agg gag ttg 350

Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu

80

85

90

95

100

105

110



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ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc tgg	446
Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp	
115 120 125	
gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg gac	494
Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp	
130 135 140	
ggt ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc acc	542
Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr	
145 150 155	
tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag ccc	590
Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro	
160 165 170	
cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag gcc	638
Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala	
175 180 185 190	
agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc aag	686
Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys	
195 200 205	
gac cag tgaccgcc accttcacac cgtctgccct ggcaccatc ctgggacctg	740
Asp Gln	
gggctgceca cagatgggca gtctcagcca tactctgttc cagctggagt agcctctga	800
ccagcctggc ccacctget ccaccactg ggeccccca gttattgata cccctctgtg	860
gtgggcctag gtaggggagg atggtgacctg gacagaggg acccacaagt gcctcccgag	1040

243/307

cctagatcct ggctcggacc actgcaaggg ccgaggcagg gccagaccag agcatcctgg 1100  
gtacaggcct gggctctcca gggcctgggc ctgattcagg tgcagtgggc actcctgaag 1160  
ggtcagagcg gcatctgcca ggcagccct ctggcttccg ctgagggtgt tgcaggcctg 1220  
gggcagagcc tgggtggta gaggcgggg ctagaggcag atggaaggga ggcatttgc 1280  
gacagaggac ggggcacccg ggtcccaact gcagtcggcc ttgctctctc ctctctctct 1340  
acctccagtc aggcctggacg ggagggtagc cttgtggctg agaggggtca gactaggtgg 1400  
cacaggggct cctggaaaga cagcaggctt cctgctgggc gttcccttgt tggagggaat 1460  
agagtggggg tgggactctg caggggtgtc cttgtccact cgcaccctc gccgccacc 1520  
agggccatgc tctgtgactt gggctgatec ccacccttc tgggcctaca gcaccacagg 1580  
ccgctgtacc cccttagagc tgcctctctc tggcctggcc ggcagacgtc ttcttaactc 1640  
ctctgtctc tatattcagc atgttccttg tcagctgctg ggccggccct gccttgcgt 1700  
agcagagcct ctctggcag cttctcaggt ctccctaatg gagacaccag gctactagga 1760  
cactggctgg ggccaccccc tctgcttaa tgcctacct tacagctggg gaaactgagg 1820  
cctggaatgg ccagagtca ccaaggcaaa gttggggctg gtcccagct gaggcctcag 1880  
ctgatgcct cagctccag agagggggtg ccccatctag ctgggtgcag gggctactgc 1940  
ttgtcagctc agggccctgt gcccgttgc ctgttccct acatctgtgc ctgcacatcc 2000  
agaactgcct ccttgcctg gccctcagga agccacctt gagccagagt caagggtgc 2060  
agcaatgcc gatagaacac gccgcctc actgctgtc ttgccttaca gccaccatgg 2120  
gaaagctgca acctttctgt tttatttaa gaaagccaa catlaaaggg tttcatgtc 2180

&lt;210&gt; 118

&lt;211&gt; 1527

&lt;220&gt;

244/307

&lt;221&gt; CDS

&lt;222&gt; (103)... (1305)

&lt;400&gt; 118

agttttccag ggcggcgggtg ggtgtccgct tctctctgct cttegactgc accgcactcg 60

cgcgtgaccc tgactccccc tagtcagctc agcgggtgctg cc atg gcg tgg cgg 114

Met Ala Trp Arg

1

cgg cgc gaa gcc agc gtc ggg gct cgc gcc gtg ttg gct ctg gcg ttg 162

Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu Ala Leu Ala Leu

5 10 15 20

ctc gcc ctg gcc ctg tgc gtg ccc ggg gcc cgg gcc cgg gct ctc gag 210

Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly Arg Ala Leu Glu

25 30 35

tgg ttc tcg gcc gtg gta aac atc gag tac gtg gac ccg cag acc aac 258

Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp Pro Gln Thr Asn

40 45 50

ctg acg gtg tgg agc gtc tcg gag agt gcc cgc ttc gcc gac agc tcg 306

Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe Gly Asp Ser Ser

55 60 65

ccc aag gag gcc gcg cat gcc ctg gtg gcc gtc ccg tgg gcg ccc gcc 354

Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro Trp Ala Pro Gly

70 75 80

85

90

95

100

245/307

ccc ggc ggc cga ggg gcc gcg ccc tgg gtc gcc ctg gtg gct cgt ggg	450
Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu Val Ala Arg Gly	
105 110 115	
ggc tgc acc ttc aag gac aag gtg ctg gtg gcg gcg cgg agg aac gcc	498
Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala Arg Arg Asn Ala	
120 125 130	
tcg gcc gtc gtc ctc tac aat gag gag cgc tac ggg aac atc acc ttg	546
Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly Asn Ile Thr Leu	
135 140 145	
ccc atg tct cac gcg gga aca gga aat ata gtg gtc att atg att agc	594
Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val Ile Met Ile Ser	
150 155 160	
tat cca aaa gga aga gaa att ttg gag ctg gtg caa aaa gga att cca	642
Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln Lys Gly Ile Pro	
165 170 175 180	
gta acg atg acc ata ggg gtt ggc acc cgg cat gta cag gag ttc atc	690
Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val Gln Glu Phe Ile	
185 190 195	
agc ggt cag tct gtg gtg ttt gtg gcc att gcc ttc atc acc atg atg	738
Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe Ile Thr Met Met	
200 205 210	
att atc tcg tta gcc tgg cta ata ttt tac tat ata cag cgt ttc cta	786
tat act ggc tct cag att gga agt cag agc cat aga aaa gaa act aag	834

246/307

Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg Lys Glu Thr Lys  
 230 235 240  
 aaa gtt att ggc cag ctt cta ctt cat act gta aag cat gga gaa aag 882  
 Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys His Gly Glu Lys  
 245 250 255 260  
 gga att gat gtt gat gct gaa aat tgt gca gtg tgt att gaa aat ttc 930  
 Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys Ile Glu Asn Phe  
 265 270 275  
 aaa gta aag gat att att aga att ctg cca tgc aag cat att ttt cat 978  
 Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys His Ile Phe His  
 280 285 290  
 aga ata tgc att gac cca tgg ctt ttg gat cac cga aca tgt cca atg 1026  
 Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg Thr Cys Pro Met  
 295 300 305  
 tgt aaa ctt gat gtc atc aaa gcc cta gga tat tgg gga gag cct ggg 1074  
 Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp Gly Glu Pro Gly  
 310 315 320  
 gat gta cag gag atg cct gct cca gaa tct cct cct gga agg gat cca 1122  
 Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro Gly Arg Asp Pro  
 325 330 335 340  
 gct gca aat ttg agt cta gct tta cca gat gat gac gga agt gat gag 1170  
 Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp Gly Ser Asp Glu  
  
 Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu Pro Gln Cys Asp

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360	365	370	
ccc agc ttt aaa gga gat gca gga gaa aat acg gca ttg cta gaa gcc			1266
Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala Leu Leu Glu Ala			
375	380	385	
ggc agg agt gac tct cgg cat gga gga ccc atc tcc tagcacac			1310
Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser			
390	395	400	
gtgcccactg aagtggcacc aacagaagtt tggettgaac taaaggacat tttatttttt			1370
ttacttttagc acataatttg tatatttgaa aataatgtat attattttac ctattagatt			1430
ctgatttgat atacaaagga ctaagatatt ttcttcttga agagactttt cgattagtcc			1490
tcatatattt atctactaaa atagagtgtt taccatg			1527

&lt;210&gt; 119

&lt;211&gt; 1905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

· 221 · CDS

· 222 · (125)... (703)

&lt;400&gt; 119

gagcctaacc tagagtgtc gcagcagtc ttcagttgag cttggggact gcagctgtgg	60
ggagatttca gtgcattgcc tcccctgggt gctcttcac ttggatttga aagttgagag	120

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tat tcc ttg ggc ctg aat gac ttg aat gtt tcc ccg cct gag cta aca	217
Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr	
20 25 30	
gtc cat gtg ggt gat tca gct ctg atg gga tgt gtt ttc cag agc aca	265
Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr	
35 40 45	
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag	313
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu	
50 55 60	
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg	361
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val	
65 70 75	
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac aac tta	409
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu	
80 85 90 95	
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag	457
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln	
100 105 110	
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc	505
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe	
115 120 125	
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa gag ctc	553
atg gtc cat gtg ggt gga ttg att cag atg gga tgt gtt ttc cag agc	601

249/307

Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser

145

150

155

aca gaa gtg aaa cac gtg acc aag gta gaa tgg ata ttt tca gga cgg 649

Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg

160

165

170

175

cgc gca aag gta aca agg agg aaa cat cac tgt gtt aga gaa ggc tct 697

Arg Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser

180

185

190

ggc tgatggtatc aggacaaagg tagaatcagg cacatgagga ggtgttgcaa 750

Gly

gagcctgggc ttgggtgctt atcagaactg gaccttctcc tagcaatttc agctttctgg 810

tgggaaagat aactccaatg aagaacaaga acaagaagat gatgatgatg cttaactttt 870

tggatgccga tatgagattg tacatgagga gattgtattt cgttactacc acaaactcag 930

gatgtctgcg gagtactccc agagctgggg ccacttccag aatcgtgtga acctgggtggg 990

ggacattttc cgaatgaag gttccatcat gcttcaagga gtgagggagt cagatggagg 1050

aaactacacc tgcagtatcc acctagggaa cctgggtgttc aagaaaacca ttgtgctgca 1110

tgtcagcccg gaagagcctc gaacactggg gaccccgcca gccctgaggc ctctgggtctt 1170

gggtggtaat cagtgggtga tcattgtggg aattgtctgt gccacaatcc tgetgctccc 1230

tgttctgata ttgatcgtga agaagacctg tggaaataag agttcagtga attctacagt 1290

cttgggtgaag aacacgaaga agactaatcc agagataaaa gaaaaacct gccattttga 1350

aagatgtgaa ggggagaaac acatttactc cccaataatt gtacgggagg tgatcgagga 1410

agaagaacca agtgaaaaat cagagggcac ctacatgacc atgcacccag ttggccttc 1470

tccgtgtgtg gtcctgggccc acctaccag tgatttcaga ctccegetct cccagctgtc 1650



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ctcctgtctc attgtttggt caatacactg aagatggaga atttggagcc tggcagagag 1710  
 actggacagc tctggaggaa caggcctgct gaggggaggg gagcatggac ttggcctctg 1770  
 gagtgggaca ctggccctgg gaaccagget gagctgagtg gcctcaaacc ccccgttgga 1830  
 tcagaccctc ctgtgggcag ggttcttagt ggatgagtta ctgggaagaa tcagagataa 1890  
 aaaccaaccc aaatc 1905

&lt;210&gt; 120

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)... (832)

&lt;400&gt; 120

gcacttgcca gccagtcgc ccgtccggag cccggctcgc tggggcagc atg gcg 55

Met Ala

1

ggg tgc cgc ctg ctc tgg ggg ccg cgg gcc ggg ggc gtc ggc ctt ttg 103

Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly Leu Leu

5

10

15

gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg ccc ccc gcg ctc tgc gcg 151

Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu Cys Ala

Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro Pro Leu

251/307

35	40	45	50	
gct gag act ggc gct cct cgc cgc ttc cgg cgg tca gtg ccc cga ggt				247
Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro Arg Gly				
	55	60	65	
	gag gcg gcg ggg gcg gtg cag gag ctg gcg cgg gcg ctg gcg cat ctg			295
	Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu			
	70	75	80	
ctg gag gcc gaa cgt cag gag cgg gcg cgg gcc gag gcg cag gag gct				343
Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala				
	85	90	95	
gag gat cag cag gcg cgc gtc ctg gcg cag ctg ctg cgc gtc tgg ggc				391
Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val Trp Gly				
	100	105	110	
gcc ccc cgc aac tct gat ccg gct ctg ggc ctg gac gac gac ccc gac				439
Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp Pro Asp				
	115	120	125	130
gcg cct gea gcg cag ctc gct cgc gct ctg ctc cgc gcc cgc ctt gac				487
Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp				
	135	140	145	
cct gcc gcc ctc gea gcc cag ctt gtc ccc gcg ccc gtc ccc gcc gcg				535
Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro Ala Ala				
	150	155	160	
	165	170	175	

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gat gct gag gag gca ggc gac gag aca ccc gac gtg gac ccc gag ctg	631
Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro Glu Leu	
180 185 190	
ttg agg tac ttg ctg gga cgg att ctt gcg gga agc gcg gac tcc gag	679
Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp Ser Glu	
195 200 205 210	
ggg gtg gca gcc ccg cgc cgc ctc cgc cgt gcc gcc gac cac gat gtg	727
Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His Asp Val	
215 220 225	
ggc tct gag ctg ccc cct gag ggc gtg ctg ggg gcg ctg ctg cgt gtg	775
Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu Arg Val	
230 235 240	
aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc ttg	823
Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu Leu	
245 250 255	
cca ccc t gagcactgcc cggatcccggt gcaccctggg acccagaagt gcccccgcca	880
Pro Pro	
260	
tcccgccacc aggactgctc cccgccagca cgtccagagc aacttacccc ggccagccag	940
ccctctcacc cgaggatccc taccctctgg ccccaata aacatgatct gaagcagc	998

C210: 121

C213: Homo sapiens

253/307

&lt;400&gt; 121

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly Ala Gly Gly Glu Pro

1 5 10 15

Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg Leu Leu Ser Ala Leu

20 25 30

Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu Val Asn Lys Ala Leu

35 40 45

Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe Leu Gly Ile Gly Gln

50 55 60

Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser Lys Leu Asn Lys Ile

65 70 75 80

Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro Val Lys Leu Phe Pro

85 90 95

Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser Gly Leu Ser Ser Thr

100 105 110

Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu Arg Lys Phe Thr Ile

115 120 125

Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu Gly Lys Gln Tyr Ser

130 135 140

Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile Leu Gly Ala Phe Ile

145 150 155 160

Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu Gly Tyr Ile Phe Val

180

185

190

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Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly Val Leu Phe Tyr Asn

195

200

205

Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile Ser Val Ser Thr Gly

210

215

220

Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp Lys Asn Val Val Phe

225

230

235

240

Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly Phe Leu Leu Met Tyr

245

250

255

Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala Leu Thr Thr Ala Val

260

265

270

Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr Ile Gly Ile Leu Ile

275

280

285

Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe Val Gly Leu Asn Ile

290

295

300

Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu Thr Leu Ser Ser Gln

305

310

315

320

Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile Cys Leu Asp Leu Lys

325

330

335

Ser

&lt;210&gt; 122

&lt;213&gt; Homo sapiens

255/307

&lt;400&gt; 122

Met Ala Glu Ala Glu Glu Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro

1 5 10 15

Arg Pro Leu Phe Ala Gly Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile

20 25 30

Pro Val Glu Gly Glu Ile Thr Ile Pro Met Arg Ser Arg Ile Arg Glu

35 40 45

Phe Asp Ser Ser Thr Leu Asn Glu Ser Val Arg Asn Thr Ile Met Arg

50 55 60

Asp Leu Lys Ala Val Gly Lys Lys Phe Met His Val Leu Tyr Pro Arg

65 70 75 80

Lys Ser Asn Thr Leu Leu Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile

85 90 95

Leu Cys Val Thr Leu Ala Leu Met Leu Gln Arg Asp Ser Ala Asp Ser

100 105 110

Glu Lys Asp Gly Gly Pro Gln Phe Ala Glu Val Phe Val Ile Val Trp

115 120 125

Phe Gly Ala Val Thr Ile Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn

130 135 140

Ile Ser Phe Phe Gln Ser Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro

145 150 155 160

Leu Thr Val Ala Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro

180

185

190

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Ala Trp Ser Ile Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro

195

200

205

Pro Asn Arg Arg Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe

210

215

220

Val Ile Ser Trp Met Ile Leu Thr Phe Thr Pro Gln

225

230

235

&lt;210&gt; 123

&lt;211&gt; 560

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg Arg Lys Thr Gly Tyr Ser

1

5

10

15

Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro Gly Arg Gly Pro Ala Gly

20

25

30

Ser Pro Ala His Leu His Thr Gly Thr Phe Trp Leu Thr Arg Ile Val

35

40

45

Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe Val Ala Phe Leu Val Ala

50

55

60

Phe His Gln Asn Lys Gln Leu Ile Gly Asp Arg Gly Leu Leu Pro Cys

65

70

75

80

Trp Glu Val Phe Ser Tyr Met Pro Thr Ile Leu Trp Leu Met Asp Trp

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100	105	110	
Ser Asp Met Asn Ser Asn Leu Asp Leu Leu Ala Leu Leu Gly Leu Gly			
115	120	125	
Ile Ser Ser Phe Val Leu Ile Thr Gly Cys Ala Asn Met Leu Leu Met			
130	135	140	
Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu Val Asn Val Gly His Val			
145	150	155	160
Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu Leu Glu Thr Gly Phe Leu			
165	170	175	
Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu Ser Arg Leu Pro Gln His			
180	185	190	
Thr Pro Thr Ser Arg Ile Val Leu Trp Gly Phe Arg Trp Leu Ile Phe			
195	200	205	
Arg Ile Met Leu Gly Ala Gly Leu Ile Lys Ile Arg Gly Asp Arg Cys			
210	215	220	
Trp Arg Asp Leu Thr Cys Met Asp Phe His Tyr Glu Thr Gln Pro Met			
225	230	235	240
Pro Asn Pro Val Ala Tyr Tyr Leu His His Ser Pro Trp Trp Phe His			
245	250	255	
Arg Phe Glu Thr Leu Ser Asn His Phe Ile Glu Leu Leu Val Pro Phe			
260	265	270	
Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile Ile His Gly Val Leu Gln			
290	295	300	



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Asn Trp Leu Thr Met Val Pro Ser Leu Ala Cys Phe Asp Asp Ala Thr  
305 310 315 320  
Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly Ser Leu Lys Asp Arg Val  
325 330 335  
Leu Gln Met Gln Arg Asp Ile Arg Gly Ala Arg Pro Glu Pro Arg Phe  
340 345 350  
Gly Ser Val Val Arg Arg Ala Ala Asn Val Ser Leu Gly Val Leu Leu  
355 360 365  
Ala Trp Leu Ser Val Pro Val Val Leu Asn Leu Leu Ser Ser Arg Gln  
370 375 380  
Val Met Asn Thr His Phe Asn Ser Leu His Ile Val Asn Thr Tyr Gly  
385 390 395 400  
Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala Glu Val Ile Leu Gln Gly  
405 410 415  
Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp Ala Met Trp Glu Asp Tyr  
420 425 430  
Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser Arg Arg Pro Cys Leu Ile  
435 440 445  
Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe  
450 455 460  
Gln Thr Tyr Glu His Asn Asp Trp Ile Ile His Leu Ala Gly Lys Leu  
465 470 475 480  
Ala Gly Arg Pro Pro Pro Arg Trp Val Arg Gly Glu His Tyr Arg Tyr

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500                      505                      510  
 Lys Phe Ser Arg Pro Gly Gly Arg His Ala Ala Glu Gly Lys Trp Trp  
 515                      520                      525  
 Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro Pro Leu Ser Leu Glu Glu  
 530                      535                      540  
 Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp Pro Leu Pro Gly Pro Leu  
 545                      550                      555                      560

&lt;210&gt; 124

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn  
 1                      5                      10                      15  
 Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu  
 20                      25                      30  
 Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg  
 35                      40                      45  
 Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile  
 50                      55                      60  
 Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val

85

90

95

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Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu

100

105

110

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly

115

120

125

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser

130

135

140

Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro

145

150

155

160

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly

165

170

175

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys

180

185

190

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met

195

200

205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr

210

215

220

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe

225

230

235

240

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly

245

250

255

Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp

260

265

270

Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln

261/307

290                      295                      300  
 Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met  
 305                      310                      315                      320  
 Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys  
                          325                      330                      335  
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys  
                          340                      345                      350  
 Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe  
                          355                      360                      365  
 Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile  
                          370                      375                      380  
 Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn  
 385                      390                      395                      400  
 Ser Glu Glu Lys Thr Lys  
                          405

&lt;210&gt; 125

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala Leu

262/307

Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly Gly Ala Val

35

40

45

Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val Gln Glu Gly His

50

55

60

Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly Glu Leu Val Leu Ala

65

70

75

80

Ser Gly Ala Gly Phe Gly Val Ser Asp Val Gly Ser His Leu Asp Cys

85

90

95

Gly Ala Gly Glu Pro Ala Val Phe Arg Asp Ser Asp Arg Phe Ser Trp

100

105

110

His Asp Pro His Leu Trp Arg Ser Gly Asp Glu Ala Pro Gly Leu Phe

115

120

125

Phe Val Asp Ala Glu Arg Val Pro Cys Arg His Asp Asp Val Phe Phe

130

135

140

Pro Pro Ser Ala Ser Phe Arg Val Gly Leu Gly Pro Gly Ala Ser Pro

145

150

155

160

Val Arg Val Arg Ser Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp

165

170

175

Glu Asp Leu Ala Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe

180

185

190

His Gly Pro Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro

195

200

205

Ala Leu Leu Gln Pro Leu Gly Gly Arg Cys Pro Gln Ala Ala Cys His

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225                      230                      235                      240  
Ser Ala Leu Arg Pro Gln Gly Gln Cys Cys Asp Leu Cys Gly Ala Val  
                         245                      250                      255  
Val Leu Leu Thr His Gly Pro Ala Phe Asp Leu Glu Arg Tyr Arg Ala  
                         260                      265                      270  
Arg Ile Leu Asp Thr Phe Leu Gly Leu Pro Gln Tyr His Gly Leu Gln  
                         275                      280                      285  
Val Ala Val Ser Lys Val Pro Arg Ser Ser Arg Leu Arg Glu Ala Asp  
                         290                      295                      300  
Thr Glu Ile Gln Val Val Leu Val Glu Asn Gly Pro Glu Thr Gly Gly  
305                      310                      315                      320  
Ala Gly Arg Leu Ala Arg Ala Leu Leu Ala Asp Val Ala Glu Asn Gly  
                         325                      330                      335  
Glu Ala Leu Gly Val Leu Glu Ala Thr Met Arg Glu Ser Gly Ala His  
                         340                      345                      350  
Val Trp Gly Ser Ser Ala Ala Gly Leu Ala Gly Gly Val Ala Ala Ala  
                         355                      360                      365  
Val Leu Leu Ala Leu Leu Val Leu Leu Val Ala Pro Pro Leu Leu Arg  
                         370                      375                      380  
Arg Ala Gly Arg Leu Arg Trp Arg Arg His Glu Ala Ala Ala Pro Ala  
385                      390                      395                      400  
Gly Ala Pro Leu Gly Phe Arg Asn Pro Val Phe Asp Val Thr Ala Ser  
  
                         420                      425                      430

264/307

Ala Asp Ser Thr Ser His Ser Tyr Phe Val Asn Pro Leu Phe Ala Gly

435

440

445

Ala Glu Ala Glu Ala

450

&lt;210&gt; 126

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu

1

5

10

15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

20

25

30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu

35

40

45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met

50

55

&lt;210&gt; 127

&lt;211&gt; 210

&lt;212&gt; PRT

Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu

265/307

1	5	10	15
Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr			
20	25	30	
Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly			
35	40	45	
Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro			
50	55	60	
Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu			
65	70	75	80
Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro			
85	90	95	
Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr			
100	105	110	
Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp			
115	120	125	
Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro			
130	135	140	
Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly			
145	150	155	160
Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser			
165	170	175	
Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr			
195	200	205	



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Gly Ser

210

&lt;210&gt; 128

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg Arg Arg Phe Leu Leu

1 5 10 15

Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu Gly Asp Ala Gly Pro

20 25 30

Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys Pro Leu Pro Arg Leu

35 40 45

Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser Ile Val Val Thr Tyr

50 55 60

Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn Phe His Thr Ser Ser

65 70 75 80

Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val Ser Leu Ser Ile Ala

85 90 95

Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys Gly Ile Gly Glu Tyr

100 105 110

Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp His Val Trp Ser Phe

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130 135 140  
 Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met Gly Val Val Met Phe  
 145 150 155 160  
 Ile Thr Leu Leu Gly  
 165

&lt;210&gt; 129

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu  
 1 5 10 15  
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln  
 20 25 30  
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala  
 35 40 45  
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe  
 50 55 60  
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly  
 65 70 75 80  
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His

100

105

110

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Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val

115

120

125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

130

135

140

His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

145

150

155

160

Arg Arg

&lt;210&gt; 130

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1

5

10

15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20

25

30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

85

90

95

269/307

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

&lt;210&gt; 131

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

atcgtgcttg tcaacaagge gctgctgacc acctacgggtt tcccgtaacc aattttcctt 180

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ggaattggac agatggcagc caccataatg atactatatg tgtccaagct aaacaaaatc 240  
 attcaattcc ctgattttga taagaaaatt cctgtaaage tgtttcctct gcctctctc 300  
 tacgttggaa accacataag tggattatca agcacaagta aattaagcct accgatgttc 360  
 accgtgctca ggaaattcac cattccactt accttacttc tggaaaccat catacttggg 420  
 aagcagtatt cactcaacat catcctcagt gtctttgccca ttattctcgg ggccttcata 480  
 gcagctgggt ctgaccttgc ttttaactta gaaggctata tttttgtatt cctgaatgat 540  
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 aaatacggag tacttttcta caatgcctgc ttcatgatta tcccaactct tattattagt 660  
 gtctccactg gagacctgca acaggtact gaattcaacc aatggaagaa tgttgtgttt 720  
 atcctacagt ttcttctttc ctgttttttg gggtttctgc tgatgtactc caeggtctc 780  
 tgcagctatt acaattcagc cctgacgaca gcagtggttg gagccatcaa gaatgtatcc 840  
 gttgcctaca ttgggatatt aatcgggtgga gactacattt tctctttgtt aaactttgta 900  
 gggttaaata tttgcatggc agggggcttg agatattcct ttttaacct gacgagccag 960  
 ttaaaccta aacctgtggg tgaagaaaac atctgtttgg atttgaagag c 1011

&lt;210&gt; 132

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

atggcggaag cggaggagtc tccaggagac ccggggacag categcccag gccctgttt 60  
 gcaggccttt cagatatatc catctcaca gacatccccg tagaaggaga aatcaccatt 120

aaaagtaata ctcttttgag agattgggat ttgtggggcc ctttgatcct ttgtgtgaca 300

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ctcgcattaa tgctgcaaag agactctgca gatagtgaag aagatggagg gcccgaattt 360  
gcagagggtgt ttgtcattgt ctggtttggg gcagttacca tcacctcaa ctcaaaactt 420  
cttggaggga acatatcttt ttttcagagc ctctgtgtgc tgggttactg tatacttccc 480  
ttgacagtag caatgctgat ttgccggctg gtacttttgg ctgatccagg acctgtaaac 540  
ttcatgggttc ggctttttgt ggtgattgtg atgtttgcct ggtctatagt tgcctccaca 600  
gcttcccttg ctgatagcca gctccaaac cgcagagccc tagctgttta tctgttttc 660  
ctgttttact ttgtcatcag ttggatgatt ctcacctta ctcctcag 708

&lt;210&gt; 133

&lt;211&gt; 1680

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

atggcggcgc ccgcggagtc gctgaggagg cggaagactg ggtaclegga tccggagcct 60  
gagtcgccgc ccgcgccggg gcgtggcccc gcaggtcttc cggcccatct ccacacgggc 120  
accttctggc tgacctggat cgtgtctctg aaggccctag ccttcgtgta cttcgtggca 180  
ttcctgggtg ctttccatca gaacaagcag ctcatcggtg acagggggct gcttccctgc 240  
agagtgttcc tgaagaactt ccagcagtac ttccaggaca ggacgagctg ggaagtcttc 300  
agctacatgc ccaccatct ctggtgatg gactggtcag acatgaactc caacctggac 360  
ttgctggctc ttctcggact ggcatctcg tctttcgtac tgatcacggg ctgcgccaac 420  
atgcttctca tggtctccct gtggggcctc tacatgtccc tggtaaatgt gggccatgtc 480  
tggtactctt tcggatggga gtcccagctt ctggagacgg ggttcttggg gatcttctg 540

ggggaccggt gctggcgaga cctcactgc atggaattcc actatgagac ccagccgatg 720

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cccaatcctg tggcatacta cctgcaccac tcaccctggt ggttccatcg cttecgagacg 780  
 etcagcaacc acttcacga gctectggig cccttcttcc tcttctcgg cggggggcg 840  
 tgcacatcc acggggtgct gcagatcctg ticcaggccg tctcatcgt cagcgggaa 900  
 etcagcttcc tgaactgget gactatggig ccagcctgg cctgcttga tgacgccacc 960  
 ctgggattct tgttccctc tgggccaggc agcctgaagg accgagttct gcagatgcag 1020  
 agggacatcc gaggggcccg gcccgagccc agattcggt cctgggtgcg gcgtgcagcc 1080  
 aacgtctcgc tgggcgtcct gctggcctgg ctccagcgc cctgggtcct caacttgctg 1140  
 agctccaggc aggtcatgaa caccacctc aactctctc acatcgtcaa cacttaagg 1200  
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 aacgccagcg ccccgatgc catgtgggag gactacgagt tcaagtcaa gccaggtgac 1320  
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 ttcgggct tccagacct cgagcacaac gactggatca tccacctggtc tggcaagctc 1440  
 ctggccagcg acccgaggc ctgtccctg ctggcacaca acccttcgc gggcaggccc 1500  
 ccgccaggt ggtccgagg agagcactac aggtacaagt tcagccgtcc tgggggcagg 1560  
 cagccgcgc agggcaagt gtgggtgcg aagaggatcg gacctactt cctccgctc 1620  
 agcctggagg agctgagcc ctacttcagg gaccgtgggt ggctctgcc cgggcccctc 1680

&lt;210&gt; 134

&lt;211&gt; 1218

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

aggcagaata ttgtctgtg gagacagccg ctactacct tgcagtattt ttctctggaa 180

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atccttgtaa tcttgaagga atggacctca aaattatggc atcgtcaaag cattgtggtg 240  
 tcttttttac tgetgcttgc tgtgcttata gctacgtatt atgttgaagg agtgcacaa 300  
 cagtatgtgc aacgtataga gaaacagttt cttttgtatg cctactggat aggcttagga 360  
 attttgtctt ctgttgggct tggaacaggg ctgcacacct ttctgcttta tctgggtcca 420  
 catatagcct cagttacatt agctgcttat gaatgcaatt cagttaattt tcccgaacca 480  
 cccatccctg atcagattat ttgtccagat gaagagggca ctgaaggaaac catttctttg 540  
 tggagtatca tctcaaaagt taggattgaa gctgcatgt ggggtatcgg tacagcaatc 600  
 ggagagctgc ctccatattt catggccaga gcagctcgcc tctcaggtgc tgaaccagat 660  
 gatgaagagt atcaggaatt tgaagagatg ctggaacatg cagagtctgc acaagacttt 720  
 gcctcccggg ccaaactggc agttcaaaaa ctagtacaga aagttggatt ttttggaaatt 780  
 ttggcctgtg cttcaattcc aaatccttta ttgtatctgg ctggaataac gtgtggacac 840  
 ttcttggtac ctttttggac ctcttttggg gcaaccctaa ttggaaaagc aataataaaa 900  
 atgcataatc agaaaatttt tgttataata acattcagca agcacatagt ggagcaaattg 960  
 gtggctttca ttgggtgctg ccccggcata ggtccatctc tgcagaagcc atttcaggag 1020  
 tacctggagg ctcaacggca gaagcttcac cacaaaagcg aaatgggcac accacaggga 1080  
 gaaaactggt tgtcctggat gtttgaaaag ttggctgttg tcatggtgtg ttacttcac 1140  
 ctatctatca ttaactccat ggcacaaagt tatgccaaac gaatccagca gcggttgaac 1200  
 tcagaggaga aaactaaa 1218

&lt;210&gt; 135

&lt;211&gt; 1359

&lt;212&gt; DNA

atggggctcc tgggcccgggt cctgtgtgtg ctgcagctct ggcactgac ccaggcggtc 60



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tccaaactct gggccccaa cacggacttc gacgtcgcag ccaactggag ccagaaccgg	120
accccggtgcg ccggcggcgc cgttgagttc ccggcggaca agatgggtgc agtcctggtg	180
caagaaggtc acgccgtctc agacatgtct ctgccgtgg atggggaact cgtcctggct	240
tcaggagccg gattcggcgt ctcagacgtg ggctcgcacc tggactgtgg cgcgggcgaa	300
cctgccgtct tccgcactc tgaccgttc tctggcatg accgcacct gtggcgctct	360
ggggacgagg cacctggcct cttcttcgtg gacgccgagc gcgtgcctg ccgccacgac	420
gacgtcttct ttccgcctag tgcctccttc cgcgtggggc tcggccctgg cgtagcccc	480
gtgcgtgtcc gcagcatctc ggctctgggc cggacgttca cgcgcgacga ggacctggct	540
gttttcttg cgtcccgccg ggcccgccct cgttccacg ggccgggcgc gctgagcgtg	600
ggccccgagg actgcgcgga cccgtcgggc tgcgtctgcg gcaacgcgga ggccgcagccg	660
tggatctgcg cggccctgct ccagccctg ggccggccgt gccccaggc cgcctgccac	720
agcgcctcc ggccccaggg gcagtgtgt gacctctgt gagccgttgt gttgtgacc	780
cacgccccg catttgacct ggagcggta cgggcgcgga tactggacac cttcctgggt	840
ctgcctcagt accacgggct gcaggtggcc gtgtccaagg tgccacgtc gtcccggtc	900
cgtgaggccg atacggagat ccaggctgtg ctggtggaga atgggcccga gacaggcgga	960
gcggggcggc tggcccgggc cctcctggcg gacgtcgcg agaacggcga ggccctcggc	1020
gtcctggagg cgacctgcg ggagtcgggc gcacacgtc ggggcagctc cgcggctggg	1080
ctggcgggcg gcgtggcggc tgccgtgtg ctggcgctgc tggctctgct ggtggcgccg	1140
ccgtctgtgc gcgcgcggg gaggtcagg tggaggaggc acgaggcggc ggccccggct	1200
ggagcgcgcc tcggttccg caaccgggtg ttcgacgtga cggcctccga ggagctgccc	1260
ctgcccggc ggctcagcct ggttccgaag gcggccgcag acagcaccag ccacagttac	1320
ttcgtcaacc ctctgttcgc cggggccgag gccgaggcc	1359

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

```

atgacctcag tttcaacaca gtgtgcttta gtctcatgt cactgctttt ggtgetgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgctg cttgggggta tatgcacgaa aaagaaatgg acagatg      177
atgacctcag tttcaacaca gtgtgcttta gtctcatgt cactgctttt ggtgetgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgctg cttgggggta tatgcacgaa aaagaaatgg acagatg      177

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&lt;210&gt; 137

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

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atggccctgc cccagatgtg tgacgggagc cacttggcct ccacctccg ctattgcatg    60
acagtcagcg gcacagtggg tctgggtggc gggacgtctt gcttcgttig gtggagcgaa    120
ggggatgcaa ccgccagcc tggccagctg gcccaccca cggagtatcc ggtgcctgag    180
ggccccagcc cctgtctcag gtccgtcagc ttgtctgtgt gcggtgcagg tgacctgtg    240
ctgtctcatg gctgtctgtg gtccgtcaag gccagcatcc cagggccacc tcgatgggac    300
ccctatcacc tctccagaga cctgtactac ctactgtgg agtctcaga gaaggagagc    360
tgcaggaccc ccaaagtggg tgacatccc acttacaggg aagccgtgag ctccctagt    420

agccttgcct ttgatgcctt ttctgcagag acgacacga gtgccacaag ctctgtctca    600

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ggcctgggttc agactgcacg gggaggaagt

630

&lt;210&gt; 138

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

atggactcct cgcgggcccg acagcagctc eggcggcgat tcctctcct gccggacgcc 60  
 gaggeccagc tggaccgcga gggtagcgc gggeccgaaa cctccacagc tgttgagaaa 120  
 aaggagaaac ctcttccaag acttaataac cattctggat tctggatttt ggcattcatt 180  
 gttgtgacct attatgttga cttctttaaa acccttaaag aaaacttcca cactagcagc 240  
 tggttctctc gtggcagtc cttgttgctt gtcagtttat caattgcatt ttactgcata 300  
 gtctacctgg aatggtattg tggaattgga gaatatgatg tcaagtatcc agccttgata 360  
 cccattacca ctgcctcctt tattgcagca ggaatttgct tcaacattgc ttatggcat 420  
 gtgtggctgt ttttactcc attgttgttg ttaccagc ttatgggggt tgcatgttt 480  
 atcacactcc ttgga 495

&lt;210&gt; 139

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

ctcttcaaca tccaggatat tgcagtcctc ttcaacatca tcatcatttt cctcatgttc 180

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ttcaacacct tegteticca ggctggcctg gtcaacctcc tattccataa gttcaaaggg	240
accatcatcc tgacagctgt gtactttgcc ctcagcatct cccctcatgt ctgggtcatg	300
aacttacgct ggaaaaactc caacagcttc atatggacag atggacttca aatgctgttt	360
gtattccaga gactagcagc agtgttgtac tgetacttct ataaacggac agccgtaaga	420
ctaggcgatc ctcacttcta ccaggactct ttgtggetgc gcaaggagtt catgcaagtt	480
cgaagg	486

&lt;210&gt; 140

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

atggcggttg cgttggcggc gctggcggcg gtcgagccgg cctgcggcag ccggtaccag	60
cagttgcaga atgaagaaga gctggagaa cctgaacagg ctgcaggta tgetcctcca	120
ccttacagca gcatttctgc agagagcgca gcataatttg actacaagga tgagtcggg	180
tttccaaagc ccccatctta caatgtagct acaacactgc ccagttatga tgaagcggag	240
aggaccaagg ctgaagctac tatccctttg gttcctggga gagatgagga ttttgtgggt	300
cgggatgatt ttgatgatgc tgaccagctg aggataggaa atgatgggat tttcatgtta	360
acttttttca tggeattcct cttaactgg attgggtttt tctgtcttt ttgcctgacc	420
acttcagctg caggaaggta tggggccatt tcaggatttg gtctctctct aattaaatgg	480
atcctgattg tcaggtttcc cacctatttc cctggatatt ttgatggta gtactggctc	540
tggtaggtgt tcttgtttt aggtttctc ctgtttctca gaggatttat caattatgca	600

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&lt;210&gt; 141

&lt;211&gt; 1622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (78)... (1091)

&lt;400&gt; 141

ctcttccccg gcccgccgg gcgggaccag tgcgcagccg gggctggcgg gcggcggggg 60

ccgcggggcc gcaggag atg acg gcc ggc ggc cag gcc gag gcc gag ggc 110

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly

1 5 10

gct ggc ggg gag ccc ggc gcg gcg cgg ctg ccc tcg cgg gtg gcc cgg 158

Ala Gly Gly Glu Pro Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg

15 20 25

ctg ctg tcg gcg ctc ttc tac ggg acc tgc tcc ttc ctc atc gtg ctt 206

Leu Leu Ser Ala Leu Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu

30 35 40

gtc aac aag gcg ctg ctg acc acc tac ggt ttc ccg tca cca att ttc 254

Val Asn Lys Ala Leu Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe

45 50 55

ctt gga att gga cag atg gca gcc acc ata atg ata cta tat gtg tcc 302

aag cta aac aaa atc att cac ttc cct gat ttt gat aag aaa att cct 350

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Lys Leu Asn Lys Ile Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro  
 80 85 90  
 gta aag ctg ttt cct ctg cct ctc ctc tac gtt gga aac cac ata agt 398  
 Val Lys Leu Phe Pro Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser  
 95 100 105  
 gga tta tca agc aca agt aaa tta agc cta ccg atg ttc acc gtg etc 446  
 Gly Leu Ser Ser Thr Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu  
 110 115 120  
 agg aaa ttc acc att cca ctt acc tta ctt ctg gaa acc atc ata ctt 494  
 Arg Lys Phe Thr Ile Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu  
 125 130 135  
 ggg aag cag tat tca ctc aac atc atc ctc agt gtc ttt gcc att att 542  
 Gly Lys Gln Tyr Ser Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile  
 140 145 150 155  
 ctc ggg gct ttc ata gca gct ggg tct gac ctt gct ttt aac tta gaa 590  
 Leu Gly Ala Phe Ile Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu  
 160 165 170  
 ggc tat att ttt gta ttc ctg aat gat atc ttc aca gca gca aat gga 638  
 Gly Tyr Ile Phe Val Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly  
 175 180 185  
 gtt tat acc aaa cag aaa atg gac cca aag gag cta ggg aaa tac gga 686  
 Val Tyr Thr Lys Gln Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly  
  
 Val Leu Phe Tyr Asn Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile

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205	210	215	
agt gtc tcc act gga gac ctg caa cag gct act gaa ttc aac caa tgg			782
Ser Val Ser Thr Gly Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp			
220	225	230	235
aag aat gtt gtg ttt atc cta cag ttt ctt ctt tcc tgt ttt ttg ggg			830
Lys Asn Val Val Phe Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly			
	240	245	250
	ttt ctg ctg atg tac tcc acg gtt ctg tgc agc tat tac aat tca gcc		878
	Phe Leu Leu Met Tyr Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala		
	255	260	265
	ctg acg aca gca gtg gtt gga gcc atc aag aat gta tcc gtt gcc tac		926
	Leu Thr Thr Ala Val Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr		
	270	275	280
	att ggg ata tta atc ggt gga gac tac att ttc tct ttg tta aac ttt		974
	Ile Gly Ile Leu Ile Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe		
	285	290	295
	gta ggg tta aat att tgc atg gca ggg ggc ttg aga tat tcc ttt tta		1022
	Val Gly Leu Asn Ile Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu		
	300	305	310
	aca ctg agc agc cag tta aaa cct aaa cct gtg ggt gaa gaa aac atc		1070
	Thr Leu Ser Ser Gln Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile		
	320	325	330

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tgtgactgcg ggetgggggg gcattcccag taggaatgtg aagccagagg ttteggattc 1180  
 gtgacatcca cccctgggc aagtgagagc atctgcaaaa tgcaaagaga actacctcat 1240  
 atgcaggatg agccaatggc agtctcaaga aatgtactcg ggcgacacct tacctgtgga 1300  
 aagcaaactt tttcaaaata agccactggg actcggtagg tggagcccca gctgctcttc 1360  
 tagggacctt tggggccttc gtggcatctc tgtgctgtgt gctggggagg aggttgatgt 1420  
 aatggtgact cttttctgat cagcaccttg gccgtgattc ccaaggtecc agccaaagca 1480  
 aagggccagt tgtttcagtt taaacagaca tgtctttagt ctaataaaat tagttaactg 1540  
 ccagtaaagt tattgttag ctttgatgaa agctatgttg gtatctttcc ctaatcatca 1600  
 aagtaaataa aaaatcattt ct 1622

&lt;210&gt; 142

&lt;211&gt; 2475

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36)... (746)

&lt;400&gt; 142

acctgtggga gcgacccggg agaaggaggg ccaag atg gcg gaa gcg gag gag 53

Met Ala Glu Ala Glu Glu

1

5

tct cca gga gac ccg ggg aca gca teg ccc agg ccc ctg ttt gca ggc 101

ctt tca gat ata tcc atc tca caa gac atc ccc gta gaa gga gaa atc 149



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Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile Pro Val Glu Gly Glu Ile  
 25 30 35  
 acc att cct atg aga tct cgc atc cgg gag ttt gac agc tcc aca tta 197  
 Thr Ile Pro Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu  
 40 45 50  
 aat gaa tct gtt cgc aat acc atc atg cgt gat cta aaa gct gtt ggg 245  
 Asn Glu Ser Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly  
 55 60 65 70  
 aaa aaa ttc atg cat gtt ttg tac cca agg aaa agt aat act ctt ttg 293  
 Lys Lys Phe Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu  
 75 80 85  
 aga gat tgg gat ttg tgg ggc cct ttg atc ctt tgt gtg aca ctc gca 341  
 Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala  
 90 95 100  
 tta atg ctg caa aga gac tct gca gat agt gaa aaa gat gga ggg ecc 389  
 Leu Met Leu Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro  
 105 110 115  
 caa ttt gca gag gtg ttt gtc att gtc tgg ttt ggt gca gtt acc atc 437  
 Gln Phe Ala Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile  
 120 125 130  
 acc ctc aac tca aaa ctt ctt gga ggg aac ata tct ttt ttt cag agc 485  
 Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser  
 Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu

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155	160	165	
att tgc cgg ctg gta ctt ttg gct gat cca gga cct gta aac ttc atg			581
Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met			
170	175	180	
gtt cgg ctt ttt gtg gtg att gtg atg ttt gcc tgg tct ata gtt gcc			629
Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala			
185	190	195	
tcc aca gct ttc ctt gct gat agc cag cct cca aac cgc aga gcc cta			677
Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu			
200	205	210	
gct gtt tat cct gtt ttc ctg ttt tac ttt gtc atc agt tgg atg att			725
Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile			
215	220	225	230
ctc acc ttt act cct cag taaatca ggaatgggaa attaaaaacc agtgaattga			780
Leu Thr Phe Thr Pro Gln			
235			
aagcacatct gaaagatgca attcaccatg gagctttgtc tctggccctt atttgtctaa			840
ttttggaggt atttgataac tgagtaggtg aggagattaa aaggagacca tatagcactg			900
tcacccctta tttaggaac tgatgtttga aaggetgttc tttctctct taatgteatt			960
tctttaaaaa tacatgtgca tactacacac agtatataat gcctccttaa ggcatgatgg			1020
agtcaccgtg gtccatttgg gtgacaacca gtgacttggg aagcacatag atacatctta			1080
caagttgaat agagttgata actattttca gttttgagaa taccagttca ggtgcagctc			1140
taggagtggg ttcatcacg gagaatgaga aaacatgeat taaccaatat tcagattttg			1320

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atcaggggaa attctacact tgttgcaaaa aaaaaaaaaa aaaaagcaaa gggcctctaa	1380
agaatcagcc tcittggtcc ctttgtgtg tcaccttttt gccatgttta acagcatctt	1440
ggttggcact ctagtcttaa tcttgtctct taactttgaa tatgcagtct aaaatgtcag	1500
tagtcaacat gtaattttcc ttgaaattc tgaatatcc agtgttgga cttatccaaa	1560
aagaagacct cagaaactta gattggtaga tctctagtgc atattatcat gtgggcacct	1620
tctcttaggg tggaatgagg cagtctggat gcagcatagt taaaaggagc tgtttaatat	1680
tctctgtagi ctggcctctt aactagaaag taaagctaaa tcagaagcct gtatttaacc	1740
atgtgaacag ggagggattt agtgttctga tggttgatta atagaacagc tagatactta	1800
gagcatgacg tgggatggga tgagtttaca gctgtgcct tttcatggg agcttagcag	1860
ttttctcatt agatgtgttt ttttgggttg gggaatagca atttatttta ttgattttag	1920
actttatcaa gctaattagc tcccccttag ataagtacat gtgcacatg tgcacctact	1980
tgtaatctca gatatttatg cacacaagtg tgaaggtttt tcaggagca gagcatctgg	2040
gacaggctga ttctgagcta aacagggtc ctttaaggca atatgaactg ttgccttcta	2100
taaattgcac attgaggaac tctaatagac aaagattagg tgtcaggcag aaaacactca	2160
ttgtaaatat actattagtt gataaacata ggactttctt attccccagt tttcttttat	2220
catataatth aaatatttat tcattttgta tttaaagact acctacacat agatatatga	2280
ttccaaagtc atactttctc catccccaca ttagccaagt gaatacaggc ccaaatgggt	2340
tcttggaatg ataataacaa agcattacaa agtgggtccc cttggttcca gccttgteca	2400
gagtttttgg ttatatattt ctatttatta caatttacct tttaaattgt aaaataaacc	2460
tttgtgtgga cagag	2475

&lt;210&gt; 143

&lt;213&gt; Homo sapiens

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)... (1703)

&lt;400&gt; 143

tgcgccctga cagcccaaca atg gcg gcg ccc gcg gag tcg ctg agg agg 50

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg

1 5 10

cgg aag act ggg tac tcg gat ccg gag cct gag tcg ccg ccc gcg ccg 98

Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro

15 20 25

ggg cgt ggc ccc gca ggc tct ccg gcc cat ctc cac acg ggc acc ttc 146

Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr Phe

30 35 40

tgg ctg acc cgg atc gtg ctc ctg aag gcc cta gcc ttc gtg tac ttc 194

Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe

45 50 55

gtg gca ttc ctg gtg gct ttc cat cag aac aag cag ctc atc ggt gac 242

Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly Asp

60 65 70

agg ggg ctg ctt ccc tgc aga gtg ttc ctg aag aac ttc cag cag tac 290

Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr

75 80 85 90

100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000

95

100

105

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ctc tgg ctg atg gac tgg tca gac atg aac tcc aac ctg gac ttg ctg	386
Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu Leu	
110 115 120	
gct ctt ctc gga ctg ggc atc tcg tct ttc gta ctg atc acg ggc tgc	434
Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly Cys	
125 130 135	
gcc aac atg ctt ctc atg gct gcc ctg tgg ggc ctc tac atg tcc ctg	482
Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu	
140 145 150	
gtt aat gtg ggc cat gtc tgg tac tct ttc gga tgg gag tcc cag ctt	530
Val Asn Val Gly His Val Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu	
155 160 165 170	
ctg gag acg ggg ttc ctg ggg atc ttc ctg tgc cct ctg tgg acg ctg	578
Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu	
175 180 185	
tca agg ctg ccc cag cat acc ccc aca tcc cgg att gtc ctg tgg ggc	626
Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu Trp Gly	
190 195 200	
ttc cgg tgg ctg atc ttc agg atc atg ctt gga gca ggc ctg atc aag	674
Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu Ile Lys	
205 210 215	
atc cgg ggg gac cgg tgc tgg cga gac ctc acc tgc atg gac ttc cac	722
tat gag acc cag cgg atg ccc aat cct gtg gca tac tac ctg cac cac	770

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Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu His His  
 235 240 245 250  
 tca ccc tgg tgg ttc cat cgc ttc gag acg ctc agc aac cac ttc atc 818  
 Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His Phe Ile  
 255 260 265  
 gag ctc ctg gtg ccc ttc ttc ctc ttc ctc ggc cgg cgg gcg tgc atc 866  
 Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile  
 270 275 280  
 atc cac ggg gtg ctg cag atc ctg ttc cag gcc gtc ctc atc gtc agc 914  
 Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile Val Ser  
 285 290 295  
 ggg aac ctc agc ttc ctg aac tgg ctg act atg gtg ccc agc ctg gcc 962  
 Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser Leu Ala  
 300 305 310  
 tgc ttt gat gac gcc acc ctg gga ttc ttg ttc ccc tct ggg cca ggc 1010  
 Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly  
 315 320 325 330  
 agc ctg aag gac cga gtt ctg cag atg cag agg gac atc cga ggg gcc 1058  
 Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg Gly Ala  
 335 340 345  
 cgg ccc gag ccc aga ttc ggc tcc gtg gtg cgg cgt gca gcc aac gtc 1106  
 Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala Asn Val  
 Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val Leu Asn

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365	370	375	
ttg ctg agc tcc agg cag gtc atg aac acc cac ttc aac tct ctt cac			1202
Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser Leu His			
380	385	390	
atc gtc aac act tac ggg gcc ttc gga agc atc acc aag gag cgg gcg			1250
Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala			
395	400	405	410
gag gtg atc ctg cag ggc aca gcc agc tcc aac gcc agc gcc ccc gat			1298
Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp			
415	420	425	
gcc atg tgg gag gac tac gag ttc aag tgc aag cca ggt gac ccc agc			1346
Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser			
430	435	440	
aga cgg ccc tgc ctc atc tcc ccg tac cac tac cgc ctg gac tgg ctg			1394
Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu			
445	450	455	
atg tgg ttc gcg gcc ttc cag acc tac gag cac aac gac tgg atc atc			1442
Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp Ile Ile			
460	465	470	
cac ctg gct ggc aag ctc ctg gcc agc gac gcc gag gcc ttg tcc ctg			1490
His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu			
475	480	485	490
495	500	505	

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gga gag cac tac agg tac aag ttc agc cgt cct ggg ggc agg cac gcc 1586

Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg His Ala

510

515

520

gcc gag ggc aag tgg tgg gtg cgg aag agg atc gga gcc tac ttc cct 1634

Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro

525

530

535

ccg ctc agc ctg gag gag ctg agg ccc tac ttc agg gac cgt ggg tgg 1682

Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp

540

545

550

cct ctg ccc ggg ccc ctc tagacgtgca ccagaaataa aggccaagac 1730

Pro Leu Pro Gly Pro Leu

555

560

ccagccccc

1739

<210> 144

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)... (1327)

<400> 144

Sequence data were obtained from

GenBank accession number

U00001.1 (Homo sapiens)

Met Ala Glu



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1

aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag gaa cat 163

Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys Glu His

5

10

15

cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag aag agg 211

His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg

20

25

30

35

agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag ccg etc 259

Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu

40

45

50

att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg aag gaa 307

Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu

55

60

65

tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct ttt tta 355

Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu

70

75

80

ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga gtg cat 403

Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His

85

90

95

caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat gcc tac 451

Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr

100

105

110

115

120

125

130

291/307

cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt aca tta	547
His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu	
135 140 145	
gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc tat cct	595
Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro	
150 155 160	
gat cag att att tgt cca gat gaa gag ggc act gaa gga acc att tct	643
Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser	
165 170 175	
ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg tgg ggt	691
Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly	
180 185 190 195	
atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc aga gca	739
Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala	
200 205 210	
gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag gaa ttt	787
Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe	
215 220 225	
gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc tcc cgg	835
Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala Ser Arg	
230 235 240	
gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt ttt gga	883
att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg gct gga	931

292/307

Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu Ala Gly  
 260 265 270 275  
 ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt ggt gca 979  
 Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe Gly Ala  
 280 285 290  
 acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa att ttt 1027  
 Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys Ile Phe  
 295 300 305  
 gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg gct ttc 1075  
 Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val Ala Phe  
 310 315 320  
 att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca ttt cag 1123  
 Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro Phe Gln  
 325 330 335  
 gag tac ctg gag gct caa egg cag aag ctt cac cac aaa agc gaa atg 1171  
 Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser Glu Met  
 340 345 350 355  
 ggc aca cca cag gga gaa aac tgg ttg tcc tgg atg ttt gaa aag ttg 1219  
 Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys Leu  
 360 365 370  
 gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac tcc atg 1267  
 Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser Met  
  
 Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu Glu

293/307

390	395	400	
aaa act aaa taagta gagaaagttt taaactgcag aaattggagt ggatgggttc			1370
Lys Thr Lys			
405			
tgccttaaatt tgggaggact ccaagccggg aaggaaaatt cccttttcca acctgtatca			1430
atTTTTacaa cttttttcct gaaagcagtt tagtecatac ttTgcactga catacttttt			1490
ccTtctgtgc taaggttaagg tateccacct cgatgcaate caccttTgtT tTcttaggg			1550
Tggaatgtga Tgttcagcag caaactTgca acagactggc cTtctgtTtg Ttactttcaa			1610
aaggeccaca tgatacaatt agagaattcc caccgcacaa aaaaagtTcc taagtatgtt			1670
aaatatgtca agctTTTTag gctTgtcaca aatgattgct TtgTTTTcct aagTcatcaa			1730
aatgtatata aattatctag attggataac agtctTgcat gTttatcatg Ttacaattta			1790
atatTccate ctgcccaccc ctTctctccc cactctcaaa aaagggecat Tttatgatgc			1850
attgcacacc ctctggggaa attgatcttt aaattTtgag acagtataag gaaaatctgg			1910
TtggTgtctt acaagtgagc Tgacaccatt Ttttattctg TgtattTaga atgaagtctt			1970
gaaaaaaact Ttataaagac atctTtaate attcc			2005

&lt;210&gt; 145

&lt;211&gt; 1558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

tcccggTcgg gtGcaaggag ccgaggcgag atg ggc gtc ctg ggc cgg gtc ctg	54
--	----

294/307

Met Gly Val Leu Gly Arg Val Leu

1

5

ctg tgg ctg cag ctc tgc gca ctg acc cag gcg gtc tcc aaa ctc tgg 102

Leu Trp Leu Gln Leu Cys Ala Leu Thr Gln Ala Val Ser Lys Leu Trp

10

15

20

gtc ccc aac acg gac ttc gac gtc gca gcc aac tgg agc cag aac cgg 150

Val Pro Asn Thr Asp Phe Asp Val Ala Ala Asn Trp Ser Gln Asn Arg

25

30

35

40

acc ccg tgc gcc ggc ggc gcc gtt gag ttc ccg gcg gac aag atg gtg 198

Thr Pro Cys Ala Gly Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val

45

50

55

tea gtc ctg gtg caa gaa ggt cac gcc gtc tea gac atg ctc ctg ccg 246

Ser Val Leu Val Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro

60

65

70

ctg gat ggg gaa ctc gtc ctg gct tea gga gcc gga ttc ggc gtc tea 294

Leu Asp Gly Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser

75

80

85

gac gtg ggc tcg cac ctg gac tgt ggc gcg ggc gaa cct gcc gtc ttc 342

Asp Val Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe

90

95

100

cgc gac tct gac cgc ttc tcc tgg cat gac ccg cac ctg tgg cgc tct 390

Arg Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val Pro

295/307

125	130	135	
tgc cgc cac gac gac gtc ttc ttt ccg cct agt gcc tcc ttc cgc gtg			486
Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe Arg Val			
140	145	150	
ggg ctc ggc cct ggc gct agc ccc gtg cgt gtc cgc agc atc tcg gct			534
Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser Ile Ser Ala			
155	160	165	
ctg ggc cgg acg ttc acg cgc gac gag gac ctg gct gtt ttc ctg gcg			582
Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala Val Phe Leu Ala			
170	175	180	
tcc cgc gcg ggc cgc cta cgc ttc cac ggg ccg ggc gcg ctg agc gtg			630
Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro Gly Ala Leu Ser Val			
185	190	195	200
ggc ccc gag gac tgc gcg gac ccg tcg ggc tgc gtc tgc ggc aac gcg			678
Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly Cys Val Cys Gly Asn Ala			
205	210	215	
gag gcg cag ccg tgg atc tgc gcg gcc ctg ctc cag ccc ctg ggc ggc			726
Glu Ala Gln Pro Trp Ile Cys Ala Ala Leu Leu Gln Pro Leu Gly Gly			
220	225	230	
cgc tgc ccc cag gcc gcc tgc cac agc gcc ctc cgg ccc cag ggg cag			774
Arg Cys Pro Gln Ala Ala Cys His Ser Ala Leu Arg Pro Gln Gly Gln			
235	240	245	
250	255	260	

ttt gac ctg gag cgg tac cgg gcg cgg ata ctg gac acc ttc ctg ggt	870
Phe Asp Leu Glu Arg Tyr Arg Ala Arg Ile Leu Asp Thr Phe Leu Gly	
265 270 275 280	
ctg cct cag tac cac ggg ctg cag gtg gcc gtg tcc aag gtg cca cgc	918
Leu Pro Gln Tyr His Gly Leu Gln Val Ala Val Ser Lys Val Pro Arg	
285 290 295	
tcg tcc cgg ctc cgt gag gcc gat acg gag atc cag gtg gtg ctg gtg	966
Ser Ser Arg Leu Arg Glu Ala Asp Thr Glu Ile Gln Val Val Leu Val	
300 305 310	
gag aat ggg ccc gag aca ggc gga gcg ggg cgg ctg gcc cgg gcc ctc	1014
Glu Asn Gly Pro Glu Thr Gly Gly Ala Gly Arg Leu Ala Arg Ala Leu	
315 320 325	
ctg gcg gac gtc gcc gag aac ggc gag gcc ctc ggc gtc ctg gag gcg	1062
Leu Ala Asp Val Ala Glu Asn Gly Glu Ala Leu Gly Val Leu Glu Ala	
330 335 340	
acc atg cgg gag tcg ggc gca cac gtc tgg ggc agc tcc gcg gct ggg	1110
Thr Met Arg Glu Ser Gly Ala His Val Trp Gly Ser Ser Ala Ala Gly	
345 350 355 360	
ctg gcg ggc ggc gtg gcg gct gcc gtg ctg ctg gcg ctg ctg gtc ctg	1158
Leu Ala Gly Gly Val Ala Ala Ala Val Leu Leu Ala Leu Leu Val Leu	
365 370 375	
ctg gtg gcg ccg ccg ctg ctg cgc cgc gcg ggg agg ctc agg tgg agg	1206
agg cac gag gcg gcg gcc ccg gct gga gcg ccc ctc ggc ttc cgc aac	1254

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Arg His Glu Ala Ala Ala Pro Ala Gly Ala Pro Leu Gly Phe Arg Asn  
 395 400 405

ccg gtg ttc gac gtg acg gcc tcc gag gag ctg ccc ctg ccg cgg cgg 1302  
 Pro Val Phe Asp Val Thr Ala Ser Glu Glu Leu Pro Leu Pro Arg Arg

410 415 420

ctc agc ctg gtt ccg aag gcg gcc gca gac agc acc agc cac agt tac 1350  
 Leu Ser Leu Val Pro Lys Ala Ala Ala Asp Ser Thr Ser His Ser Tyr

425 430 435 440

ttc gtc aac cct ctg ttc gcc ggg gcc gag gcc gag gcc t gagcgccgc 1400  
 Phe Val Asn Pro Leu Phe Ala Gly Ala Glu Ala Glu Ala

445 450

ctgaccgtcg accttgggge tctccacccc ctctggcccc agtcgaactg ggggctagcc 1460  
 acctctctgt ccagccccca aacctcccct tcttttcccc ctctccggg ggccaaggac 1520  
 aggttgccct tactcagtaa aggtgtttcc tgcacctg 1558

&lt;210&gt; 146

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (151)... (330)

ccggagctcc aggaaggga aatttcaagt cagatagaat tetatatata ccatttcttt 120



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ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg 174

Met Thr Ser Val Ser Thr Gln Leu

1

5

tcc tta gtc ctc atg tca ctg ctt ttg gtg ctg cct gtt gtg gaa gca 222

Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala

10

15

20

gta gaa gcc ggt gat gca atc gcc ctt ttg tta ggt gtg gtt ctc agc 270

Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser

25

30

35

40

att aca ggc att tgt gcc tgc ttg ggg gta tat gca cga aaa aga aat 318

Ile Thr Gly Ile Cys Ala Cys Leu Gly Val Tyr Ala Arg Lys Arg Asn

45

50

55

gga cag atg tga ctttgaaagg cctactgagt caaacctcac cctgaaaacc 370

Gly Gln Met

tttgcgttt agaggctaaa cctgagattt ggtgtgtgaa aggttccaag aatcagtaaa 430

taaggagatt tcacattttt cattgtttcc atgaaatggc aacaaacata catttataaa 490

ttgaaaaaaaa aatgttttct ttacaacaaa taatgcacag aaaaatgcag cctataattt 550

gctagttagg tagtcaaaga agtaagatgg ctgaaattta cataagtaat atttcataat 610

cttagaattc tctcaaagca tgtgaaatag gaagaaggaa gttcttgccc agaattcttag 670

gaaatcacca ctgttcgggtt ataatactg cctcctgaat cgttgaggag tctttttaat 730

tagatttttg ttttgttgtc tcccaagtta atattatatt tagatatcag agagtcagge 790

aaaaaggaaa acttttatct ctagggaataa aacatttaga aaaatgtatt cagtgtatct 850

ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg

gaagtactat attaaatata aaccattat gttat

1005

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&lt;210&gt; 147

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (151)...(783)

&lt;400&gt; 147

gctggacacc tggagctgcc cgaggacgcg gaggagagac ccgagggctcg ccgctggtag 60

ggtogetcag cctgcccgc cttcaccacc acacctcac ctgcgccag ctccctgcgc 120

gcctggacag cgctgctgc ccgcctcccg atg gcc ctg ccc cag atg tgt gac 174

Met Ala Leu Pro Gln Met Cys Asp

1

5

ggg agc cac ttg gcc tcc acc ctc cgc tat tgc atg aca gtc agc ggc 222

Gly Ser His Leu Ala Ser Thr Leu Arg Tyr Cys Met Thr Val Ser Gly

10

15

20

aca gtg gtt ctg gtg gcc ggg acg ctc tgc ttc gct tgg tgg agc gaa 270

Thr Val Val Leu Val Ala Gly Thr Leu Cys Phe Ala Trp Trp Ser Glu

25

30

35

40

ggg gat gca acc gcc cag cct ggc cag ctg gcc cca ccc acg gag tat 318

Gly Asp Ala Thr Ala Gln Pro Gly Gln Leu Ala Pro Pro Thr Glu Tyr

Pro Val Pro Glu Gly Pro Ser Pro Leu Leu Arg Ser Val Ser Phe Val

300/307

60	65	70	
tgc tgc ggt gca ggt ggc ctg ctg ctg ctc att ggc ctg ctg tgg tcc			414
Cys Cys Gly Ala Gly Gly Leu Leu Leu Leu Ile Gly Leu Leu Trp Ser			
75	80	85	
gtc aag gcc agc atc cca ggg cca cct cga tgg gac ccc tat cac ctc			462
Val Lys Ala Ser Ile Pro Gly Pro Pro Arg Trp Asp Pro Tyr His Leu			
90	95	100	
tcc aga gac ctg tac tac ctc act gtg gag tcc tca gag aag gag agc			510
Ser Arg Asp Leu Tyr Tyr Leu Thr Val Glu Ser Ser Glu Lys Glu Ser			
105	110	115	120
tgc agg acc ccc aaa gtg gtt gac atc ccc act tac gag gaa gcc gtg			558
Cys Arg Thr Pro Lys Val Val Asp Ile Pro Thr Tyr Glu Glu Ala Val			
125	130	135	
agc ttc cca gtg gcc gag ggg ccc cca aca cca cct gca tac cct acg			606
Ser Phe Pro Val Ala Glu Gly Pro Pro Thr Pro Pro Ala Tyr Pro Thr			
140	145	150	
gag gaa gcc ctg gag cca agt gga tcg agg gat gcc ctg ctc agc acc			654
Glu Glu Ala Leu Glu Pro Ser Gly Ser Arg Asp Ala Leu Leu Ser Thr			
155	160	165	
cag ccc gcc tgg cct cca ccc agc tat gag agc atc agc ctt gct ctt			702
Gln Pro Ala Trp Pro Pro Pro Ser Tyr Glu Ser Ile Ser Leu Ala Leu			
170	175	180	
185	190	195	200

301/307

ggc ctg gtt cag act gca cgg gga gga agt taaaggctcc tagcaggctcc 800

Gly Leu Val Gln Thr Ala Arg Gly Gly Ser

205

210

tgaatccaga gacaaaaatg ctgtgccttc tccagagtct tatgcagtgc ctgggacaca 860

gtaggcactc agcaaacggt cgttggtgaa ggctgttcta tttatctatt gctgtataac 920

aaaccacccc agaatttagt ggcttaaaat aaatcccatt ttattatgt 969

<210> 148

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)... (517)

<400> 148

atttcggggc ggtaccaag atg gac tcc tcg cgg gcc cga cag cag ctc cgg 52

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg

1

5

10

cgg cga ttc ctc ctc ctg ccg gac gcc gag gcc cag ctg gac cgc gag 100

Arg Arg Phe Leu Leu Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu

15

20

25

ggc gac gcc ggg ccg gaa acc tcc aca gct gtt gag aaa aag gag aaa 148

cct ctt cca aga ctt aat atc cat tct gga ttc tgg att ttg gca tcc 196

302/307

Pro Leu Pro Arg Leu Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser  
 45 50 55  
 att gtt gtg acc tat tat gtt gac ttc ttt aaa acc ctt aaa gaa aac 244  
 Ile Val Val Thr Tyr Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn  
 60 65 70 75  
 ttc cac act agc agc tgg ttt ctc tgt ggc agt gcc ttg ttg ctt gtc 292  
 Phe His Thr Ser Ser Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val  
 80 85 90  
 agt tta tca att gca ttt tac tgc ata gtc tac ctg gaa tgg tat tgt 340  
 Ser Leu Ser Ile Ala Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys  
 95 100 105  
 gga att gga gaa tat gat gtc aag tat cca gcc ttg ata ccc att acc 388  
 Gly Ile Gly Glu Tyr Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr  
 110 115 120  
 act gcc tcc ttt att gca gca gga att tgc ttc aac att gct tta tgg 436  
 Thr Ala Ser Phe Ile Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp  
 125 130 135  
 cat gtg tgg tgg ttt ttc act cca ttg ttg ttg ttt acc cag ttt atg 484  
 His Val Trp Ser Phe Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met  
 140 145 150 155  
 ggg gtt gtc atg ttt atc aca ctc ctt gga tgattt ccgaagagac 530  
 Gly Val Val Met Phe Ile Thr Leu Leu Gly  
 -----  
 tcagccttcg aagtagttgg gactacaggc ccagccacc gtgcctgget ggacatgtaa 650

303/307

atttgaagtg aatgggttaa catccagcta gctgaaagca tggcagaccc taacagaaaa 710  
 gctacagtgt gtttttgcag ctatgaagtg aatggtttcc tggggaaaat tgtgactttg 770  
 tataactgtt gttgaaacca gaataaatta tatttcactt gcatatgcat aaattattaa 830  
 aattttcaga agtcagtgat acagaagtac tattttgcaa tgttaatctg ttgagtcctt 890  
 tggagaaagt ggtttcattg taggtacata gtgcactgtt aatattttta acaagtagtt 950  
 cactcttcca ttttaaggat agcagttcct tgtataaaat gactggatgt gtataaagga 1010  
 attatgttgt catgtgcctt taaccagctt tagtaattac tataatctca tatttatgat 1070  
 agttttgtta ggtgacagga ccaaatgaaa atattttatg ttttctcatc actttagatt 1130  
 ttatcattat gtacattact gggtttttag catttcttaa tgtgaagttt taatcacttt 1190  
 taagtataca tttttttctg tatcatttaa ataaaatatt tttataactt t 1241

&lt;210&gt; 149

&lt;211&gt; 1174

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (187)... (675)

&lt;400&gt; 149

ggaagccggg acgatgtccg catgacaacc gacgttggag ttggaggtg cttgccttag 60  
 agcaaggga acagctctca ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga 120  
 cagccaggag cggttttctg ggaactgtgg gatgtgccct tgggggcccg agaaaacaga 180

304/307

ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc tca gaa ctg	276
Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu	
15 20 25 30	
ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc atc cag gat	324
Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp	
35 40 45	
att gca gtc ctc ttc aac atc atc atc att ttc ctc atg ttc ttc aac	372
Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn	
50 55 60	
acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc cat aag ttc	420
Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe	
65 70 75	
aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc agc atc tcc	468
Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser	
80 85 90	
ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc aac agc ttc	516
Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe	
95 100 105 110	
ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag aga cta gca	564
Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala	
115 120 125	
gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta aga cta ggc	612
gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag gag ttc atg	660

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Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met

145

150

155

caa gtt cga agg tgacctct tgtcacactg atggatactt ttccttcctg

710

Gln Val Arg Arg

160

atagaagcca catttgctgc ttgacagga gagttggccc tatgcatggg caaacagctg 770

gactttccaa ggaagggtca gactagctgt gttcagcatt caagaaggaa gatcctccct 830

cttgacaaat tagagtgtcc ccacgggtct ccagtgggc atcccttctt tgccttctac 890

ctctgttcca ccccttttcc ttccttttct ctctgtacca ttcattctcc ctgaccggcc 950

tttcttgccg agggttctgt ggctcttacc ctgtgaage tttccttta gcctgggaca 1010

gaaggacctc ccagccccca aaggatctcc cagtaccaa aggatgcgaa gagtgatagt 1070

tacgtgctcc tgactgatca caccgcagac atttagattt ttatacccaa ggcacttta 1130

aaaaatgttt tataaataga gaataaattg aattcttgtt ccat 1174

&lt;210&gt; 150

&lt;211&gt; 1012

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (208)... (873)

&lt;400&gt; 150

aagagcgtct cgcgcgggag cggcggcggc cctcgagacc caaccaagga ggcctccctt 120

cgccctccca gcctcccaaa gcgcagcggc ccgcgccctt tcagctagct cgctcgtctg 180



306/307

ctctgcttcc ctgctgccgg ctgcgcc atg gcg ttg gcg ttg gcg gcg ctg 231

Met Ala Leu Ala Leu Ala Ala Leu

1

5

gcg gcg gtc gag ccg gcc tgc gcc agc cgg tac cag cag ttg cag aat 279

Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn

10

15

20

gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct cca 327

Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro

25

30

35

40

cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac aag 375

Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys

45

50

55

gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca aca 423

Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr

60

65

70

ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act atc 471

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile

75

80

85

cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat ttt 519

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe

90

95

100

gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg tta 567

act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg tct 615

307/307

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser  
 125 130 135  
 ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca gga 663  
 Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly  
 140 145 150  
 tt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc acc 711  
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr  
 155 160 165  
 tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg ttc 759  
 Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe  
 170 175 180  
 ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat gca 807  
 Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala  
 185 190 195 200  
 aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc aga 855  
 ys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg  
 205 210 215  
 gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg catttatgaa 910  
 Val Leu Phe Ile Tyr  
 220  
 ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca gaacacagag 970  
 aaataatcag ctgctttcag aaataaagt actgttgaaa ag 1012